

Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.

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tggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750
cagatccagt aaaggttaatt gaaaaaaaaac tcgccatttggagcagctg 800
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taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature

<222> 36-47, 108-113, 166-171, 198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10

Met	Leu	Phe	Trp	Val	Leu	Gly	Leu	Leu	Ile	Leu	Cys	Gly	Phe	Leu
1				5					10				15	
Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys
					20				25				30	
Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
					35			40				45		
Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
					50			55				60		
Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
					65				70			75		
Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80				85				90		
Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95				100				105		
Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115			120		
Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125				130				135		
Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145			150		
Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155				160				165		
Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Tyr	Thr	Pro	Ser	Lys	
				170				175				180		
Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185				190				195		

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
 200 205 210
 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
 215 220 225
 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
 230 235 240
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
 245 250 255
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
 260 265 270
 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
 275 280 285
 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
 290 295 300
 Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
 305 310 315
 Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapines

<400> 11
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 gccccttggg ccgtcgccac cactgttagtc atgtaccac cgcgcgcgc 150
 gcccctcat cgggacttca tctcggtgac gctgagctt ggcgagagct 200
 atgacaacag caagagttgg cggccgcgcgt cgtgctggag gaaatggaaag 250
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 gggtaaaaac cagcaaatcc acccgcttta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacacagaag acacaaagac 500
 acatccagcg gggaccacct cacatgcaga tttagaccccc aagccaagac 550
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gagcgggtgat cgagcctgag cagggcacccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccacccg gccaggacac agggcacacc 750
agtgcacatctg aactatcgcc agaagggcgt gattgacgac ttcctgcata 800
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
gtgtccaggt ctttcagtga gtgggttggc ctcggtctca cactgatcga 900
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cagtcttgggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350
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ttgatttgct ctaaccgcaa 2720

<210> 12
<211> 699
<212> PRT
<213> Homo sapiens

<220>
<221> TRANSMEM
<222> 21-40 and 84-105
<223> Transmembrane Domain (type II)

<400> 12
Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
20 25 30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
35 40 45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
50 55 60
Asp Asn Ser Lys Ser Trp Arg Arg Ser Cys Trp Arg Lys Trp
65 70 75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
80 85 90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
95 100 105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
 110 115 120
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
 125 130 135
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
 140 145 150
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
 155 160 165
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
 170 175 180
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
 185 190 195
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
 200 205 210
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
 215 220 225
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
 230 235 240
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
 245 250 255
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
 260 265 270
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
 275 280 285
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
 290 295 300
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
 305 310 315
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu
 320 325 330
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu
 335 340 345
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn
 350 355 360
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser
 365 370 375
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr
 380 385 390
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala 410	415	420
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys 425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe 440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr 455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu 470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg 485	490	495
Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val 500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu 515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly 530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr 545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu 560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val 575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr 590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys 605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe 620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln 635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe 650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp 665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala 680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 13

cgccagaagg gcgtgattga cgtc 24

<210> 14

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 14

ccatccttct tcccagacag gccg 24

<210> 15

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 15

gaagcctgtg tccaggtcct tcagttagtg gtttggcctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

ggcgccgcgt aggccccggga ggccggggccg gcccggctgc gagcgcctgc 50

cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gagaaaagcg 100

gcccgcgtgc cctgggagga cggcaggatcc gggttgtctt ccggcggcct 150

ccctcggaag tggccgtct tccacctgtt cgtggcctgc ctctcgctgg 200

gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggccctc cccgtgcctg 300
ccccccagag cgccccctg agcaactggga agaagacgca tcctgggccc 350
cccaccgcct ggcagtgctg gtgcccttcc gogaacgcctt cgaggagctc 400
ctggtcttcg tgccccacat gogccgcttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtggc ttcctggaga gcagcaacag cacggactac 550
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
tggctttcct gaggctggc cttccacgt ggcctcccg gagctccacc 650
ctctctacca ctacaagacc tatgtcggcg gcatcctgct gctctccaag 700
cagcactacc ggctgtcaa tggatgtcc aaccgcttct gggctgggg 750
ccgcgaggac gacgagtctt accggcgcat taagggagct gggctccagc 800
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tgaacaggac aacctctcat caccccaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-42

<223> Signal peptide.

<220>

<221> misc_feature

<222> 19-25,65-71,247-253,285-291,303-310

<223> N-myristoylation site.

<220>

<221> misc_feature

<222> 27-31

<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>

<221> TRANSMEM

<222> 29-49

<223> Transmembrane domain (type II).

<220>

<221> misc_feature

<222> 154-158

<223> N-glycosylation site.

<220>

<221> misc_feature

<222> 226-233

<223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp
1				5					10				15	

Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser
				20					25				30	

Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser
					35				40				45	

Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala
				50					55				60	

Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys
					65				70				75	

Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp
					80				85				90	

Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe
				95					100				105	

Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser
				110					115				120	

Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp
				125					130				135	

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp		
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala		
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
tttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccgaaaa gtctttctg ccactgacgc ccccatcagg 150
gattgggcct tcttcccccc ttcccttctg tgtctcctgc ctcatcgccc 200
tgccatgacc tgcagccaag cccagccccg tggggaaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggcttaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacagttt aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccc ctgggcccgc gccgcgcctcc tgcccgcccc 150

ggctccgggg cgccccgcta ggccagtgcg ccgcgcctcg cccgcaggc 200

cccgccccgc agcatggagc cacccggacg ccggcggggc cgcgccgcgc 250

cgccgcgttt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300

ggccgcggcg gcggcggcgc cgccgcgtg cccgcggct gcaagcacga 350

tggcggccc cgaggggctg gcagggcggc gggccgcgc gaggcaagg 400

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cccaaccgca cggtcacccct gattctgagt aacaataaga tatccgagct 500

gaagaatggc tcattttctg gtttaagtct ctttggaaaga ttggacctcc 550

gaaacaatct tatttagtg atagatccag gtgccttctg gggactgtca 600

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agacatattt cgaggactca ccaatctggc tcggctaaac ctttcgggga 700

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<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

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35 40 45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
 110 115 120
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe		
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val		
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr		
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu		
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu		
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys		
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu		
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala		
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg		
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile		
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met		
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly		
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys		
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu		
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr		
605	610	615

Ser

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<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24

<223> Synthetic construct

<400> 25
gaggactcac caatctggtt cggc 24

<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 26
aactggaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 27
gtaaaaggaga agaacatcac ggtacggat accaggtgtg tttatcctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcggta 150
aaaaagaaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattt gcaaaaggat ctcaaaaatc 250
atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatctt tttttggtc 350
actgtcccttt taaacctgtat caaataaagg acagtgggtc atataagtta 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
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gtggagggag agacgctcct gatcgctgaa tcc 683

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<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-21
<223> Signal peptide.

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Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45

Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60

Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
65 70 75

Lys Gly Ser Gln Lys Ser
80

<210> 30
<211> 2128
<212> DNA
<213> Homo sapiens

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tccgtggatt cctctgtcaa gaccgctgcc atgccagtga cggttaacccg 150
caccaccatc acaaccacca cgacgtcatc ttccggcctg gggccccca 200
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<210> 31
<211> 322
<212> PRT
<213> Homo sapiens

<400> 31
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35 40 45
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105
Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
110 115 120
Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
125 130 135
His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
140 145 150
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
155 160 165
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
170 175 180
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
185 190 195
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
 215 220 225
 Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
 230 235 240
 Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
 245 250 255
 Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
 260 265 270
 Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
 275 280 285
 Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
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 His Leu Val Phe Val Lys Val
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 <210> 32
 <211> 3680
 <212> DNA
 <213> Homo sapiens

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taatataaaa atctttgtAA atctctaaaa 3680

<210> 33
<211> 335
<212> PRT
<213> Homo sapiens

<400> 33
Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
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Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
20 25 30
Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
35 40 45
His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
50 55 60
Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
65 70 75
Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
80 85 90
Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
95 100 105
Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
110 115 120
Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330
Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtcctttgt cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccc tcgcgatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgcgtggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
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ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150
tgatatttca gttcctgatt gtaaataacct cctaaggctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaaat gggcataata 250
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aataccaaag aagcctacaa tggtggcctt agccaaaatt ctgttgattt 350
caacgttgtt ttatttcactt ctatcgaaaa gccatggaaa agaaaatcaa 400
gacataaaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
atataaccac ctcaaatactc aaggcgagtc attccccctcc tttgaatcta 550
cccaacaaca gccacggaat aacagattc tccagtaact catcagcaga 600
gcattcttg ggcagtctaa aacccacatc taccatttcc acaagccctc 650
ccttcatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700
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ctgataacag ttccattaca gtttagcatcc tctcttcaga accaacttct 850
ccatctgtga ccccccttgat agtggAACCA agtggatggc ttaccacaaa 900
cagtgatagc ttcactgggt ttacccctta tcaagaaaaa acaactctac 950
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aggtgctatt ctgggtgtct cattgcttac tcttgtggc tacttggtgt 1100
gtggaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150
agaaatgaac cagttctgcg attagacaat gcaccggAACCTT cttatgatgt 1200
gagttttggg aattctagct actacaatcc aactttgaat gattcagcca 1250
tgccagaaag tgaagaaaaat gcacgtgatg gcattcctat ggatgacata 1300
cctccacttc gtacttctgt atagaactaa cagaaaaag gcgttaaaca 1350
gcaagtgtca tctacatcct agcctttga caaattcatc tttcaaaagg 1400
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acctgtattc tagtacgtta taatttcta gatcagcaca cacatgatca 1900
gcccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agttcttta aaagtcttca 2000
aagggttgg gaatttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

Met	Leu	Ala	Leu	Ala	Lys	Ile	Leu	Leu	Ile	Ser	Thr	Leu	Phe	Tyr
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Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
				20				25						30
Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
		35						40						45
Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
		50						55						60
Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
		65					70							75
Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
		80					85							90
Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
		95					100							105
Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val
		110					115							120
Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser
		125					130							135
Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr
		140					145							150
Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser
		155					160							165
Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val
		170					175							180
Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser
		185					190							195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
		200				205						210		
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
	215					220						225		
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
		230					235					240		
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
		245					250					255		
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
		260					265					270		
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
		275					280					285		
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
		290					295					300		
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
		305					310					315		
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
		320					325					330		
Arg	Thr	Ser	Val											

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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 ccccttaccgc cgtgcaaaag gagggaggcgc ggcaagacgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gtcctctgg gagatgtatg cttactctct 250
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 ttttGattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
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ttccgccttc gtcgcagaga cctcttgctg ggttcaaca aacgtgccat 800
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtcaga gatttacaat atgactttaa cattaagggt tatggatac 950
tcaagatatt tactcatgca tttactctat tgcttatgct taaaaaaaaag 1000
aaaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050
taattggcat tgcttgttt ttgaaactga aattacatga gtttcatttt 1100
ttcttgcattt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgttttttt gttgtttgt 1200
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ttaacctgac ttatatgtga acaattttca tgagacagtc attttaact 1450
aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
tgtgttaggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550
ccctataata aattttactc tataaaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30

Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45

Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly	Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg	Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser	Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp	Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro	Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe	Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys	Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn	Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln	Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile	Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn	Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly	Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe	Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgAAC cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggggcag ggcgcagccc agagcagccc cgggcaccag 50

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gttgcggcgg cagccccag ctcctcatc ttctgttgc tgctgctggg 200
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250
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ggcaggaggt cctctcccccc atccctccat ctggggctcc cccaacctct 1850
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaa 1950
aaaaaaaaaaa aaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu
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Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
20 25 30
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr
				170					175					180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp
				185				190			195			
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys
				200				205			210			
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro
				215				220			225			
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu
				230				235			240			
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly
				245				250			255			
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro
				260				265			270			
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val		
				275				280						

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
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 gcacagagac gcagagcaag ggcggcaagg aggagacctt ggtggagga 150
 agacactctg gagagagagg gggctggca gagatgaagt tccagggcc 200
 cctggcctgc ctccctgctgg ccctctgcct gggcagtggg gaggtggcc 250
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 ggacatggcc tgggagacgc cctgagcgaa ggggtggaa aggccattgg 350
 caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccattggcc 400
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggctt 450
 ggcgcagcag atgctttggg caacagggtc gggaaagcag cccatgctct 500
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tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc 1500
ccgtgacctc cagacaagga gccaccagat tggatggag ccccccacact 1550
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aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1734

<210> 52
<211> 440
<212> PRT
<213> Homo sapiens

<400> 52
Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
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20 25 30
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
35 40 45
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
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Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser
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<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

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<211> 280

<212> PRT

<213> Homo sapiens

<400> 54

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Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
			80				85					90		
Ile	Thr	Pro	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln	
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Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
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Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
			125				130					135		
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Ala	Asp	Leu	Val	Arg	Gln	Ala	Glu	Ser	Leu	Leu	Gln	Glu	Gln	Leu
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Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
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Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
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Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
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Ala	Leu	Leu	Pro	Glu	Glu	Thr	Pro	Ala	Ala	Val	Leu	Ser	Ser	Ala
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Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
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Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
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Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
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<212> DNA
<213> Homo sapiens

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<210> 56
<211> 299
<212> PRT
<213> Homo sapiens

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Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly
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Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val
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Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro
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Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp
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cctacactcg tggcatcagt ggacgggcgt gtgctaattgg gatccacatg 3150
aataggggct gcccctcgcc tgcaagtggc tacccgggca tgaagcccc 3200
gcagcactgc ccaggcgagc ttcagcagca gagtgacacc agcagcctgc 3250
tgagggcagac ccattttggc aatggatatg accccccaaag tcaccagatc 3300
acgagggggtc ccaagtcttag cccggacgag ggcttttct tatacacact 3350
gcccggacgac tccactcacc agctgctgca gccccatcac gactgctgcc 3400
aacggccagga gcagcctgct gctgtggcc agtcaggggt gaggagagcc 3450
cccgacagtc ctgtcctgga agcaagtgtgg gaccctccat ttcactcagg 3500
gccccatgc tgcttggcc ttgtgccagt tgaagaggtg gacagtccctg 3550
actcctgcca agtgagtgga ggagactggt gtccccagca ccccgtaggg 3600
gcctacgtag gacaggaacc tggaatgcag ctctccccgg ggccactggt 3650
gcgtgtgtct tttgaaacac cacctctcac aatttaggca gaagctgata 3700
tcccagaaag actatatatt gtttttttttaaaaaaaaaa agaagaaaaaa 3750
agagacagag aaaattggta tttattttc tattatagcc atatttat 3800
atttatgcac ttgtaaataa atgtatatgt tttataattc tggagagaca 3850
taaggagtc taccctgtga ggttggagag ggaaaataaa gaagctgcc 3900
cctaacagga gtcacccagg aaagcaccgc acaggctggc gcgggacaga 3950
ctcctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000
agataagctg gcaagaggaa ggatcccagg cacatggtc atcacgagca 4050
tgagggaaaca gcaaggggca cggtatcaca gcctggagac acccacacag 4100
atggctggat ccggtgctac gggaaacatt ttcctaagat gcccatgaga 4150
acagaccaag atgtgtacag cactatgagc attaaaaaaac cttccagaat 4200
caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250
aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58
<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu
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Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala
		20					25					30		
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr
		35					40				45			
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu
		50					55				60			
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu
		65					70				75			
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr
		80					85				90			
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln
		95					100				105			
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
		110					115				120			
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln
		125					130				135			
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys
		140					145				150			
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val
		155					160				165			
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met
		170					175				180			
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu
		185					190				195			
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val
		200					205				210			
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr
		215					220				225			
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile
		230					235				240			
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser
		245					250				255			
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser
		260					265				270			

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
 275 280 285
 Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met
 290 295 300
 Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr
 305 310 315
 Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
 320 325 330
 Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
 335 340 345
 Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
 350 355 360
 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
 365 370 375
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
 395 400 405
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
 410 415 420
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
 425 430 435
 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
 530 535 540
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys		Glu Gln Gln Ile Gln	
575	580	585	
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp			
590	595	600	
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile			
605	610	615	
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg			
620	625	630	
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys			
635	640	645	
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile			
650	655	660	
Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly			
665	670	675	
Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu			
680	685	690	
Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr			
695	700	705	
Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr			
710	715	720	
Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met			
725	730	735	
Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr			
740	745	750	
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys			
755	760	765	
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His			
770	775	780	
Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn			
785	790	795	
Glu Gly Gly Glu Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr			
800	805	810	
Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro			
815	820	825	
Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg			
830	835	840	
Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro			
845	850	855	

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile
					860				865				870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln
					875				880				885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro
					890				895				900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His
					905				910				915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala
					920				925				930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala
					935				940				945	
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu
					950				955				960	
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His
					965				970				975	
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly
					980				985				990	
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro
					995				1000				1005	
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys
					1010				1015				1020	
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg
					1025				1030				1035	
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro
					1040				1045				1050	
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu
					1055				1060				1065	
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp
					1070				1075				1080	
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly
					1085				1090				1095	
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr
					1100				1105				1110	
Pro	Pro	Leu	Thr	Ile										
					1115									

<210> 59
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcatcg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgttag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccccaaag cccaggatccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cggggaggctg ggtcgcatg atccggaccc cattgtcgcc ctctgccc 50
cgcctgctcc tccccaggctc ccgcggccga ccccccgcga acatgcagcc 100
cacgggccgc gaggggttccc gcgcgcgtcag cccggcgat ctgcggcg 150
tgctgctcct gctactgctg ctgctgctgc ggcagcccgta aaccgcgcg 200
gagaccacgc cgggcgcggc cagagccctc tccacgctgg gtcggcc 250
cctcttcacc acgcccgggtg tccccagcgc cctcaactacc ccaggccta 300
ctacgccagg caccccaaaa accctggacc ttccgggtcg cgccgaggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
gcccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
cctactctga actcgagctt gtgacacctag ctgaaggctt gaacagctct 650
caaaagctgg cctgcctcat tggcgtgnag ggtggtaact cactggacag 700
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
caacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcggta ttgacaagct ttggtgagaa 850
agtagtagag gagttgaacc gcctggcat gatgatacat ttgtcctatg 900
catcgacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950
atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
tcccgatgat atcctgcagc ttctgaagaa cggtggcatc gtgatggta 1050
caactgtccat ggggtgctg cagtcaacc tgcttgctaa cgtgtccact 1100
gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150
cgggatttgtt ggaaattatg acgggactgg ccggttccct caggggctgg 1200
aggatgtgtc cacataccca gtcctgatag aggagttgtc gagtcgtasc 1250
tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
tggaggctga gtttccatat gggcaactga gcacatcctg ccactccac 1400
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
gccaaaccaat cgggtccctt ggaggtcctc aaatgcctcc ccatacctt 1500
ttccaggccct tgtggctgtc gccaccatcc caaccttcac ccagtggctc 1550
tgctgacaca gtcggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> 196, 386
<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg
1				5				10					15	
Tyr	Leu	Arg	Arg	Leu	Arg									
	20							25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
		35				40						45		
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
		50						55				60		
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro
		65				70					75			
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser
		80				85						90		
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg
		95					100					105		
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe
		110					115					120		
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val
		125				130					135			
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp
		140				145					150			
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His
		155				160					165			
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala
		170				175					180			
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val
		185					190					195		
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser
		200				205					210			
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys
		215				220					225			
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met
		230				235					240			
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
		245				250					255			
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tggc 25
<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
gtcacacaca gctctggcag ctgag 25
<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaaggc 47
<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
tgctaggctc tgtcccacaa tgcaccccgag agcaggagct gaaaggctct 50
aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccgacaa gcctgataag catgaagctc ttatcttgg tggctgtgg 150
cgggtgtttt ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccacccctata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtgaa tgccctgttg ctctacatgg ctttcctgat 450
gctgggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgaaa gaccccgagc aaacacagtc ctggagcgtg tgaaagggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaaag acagtcttcg 650
 atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
 ccaacaccat ggctgccagc ttccaggctg gacaaagcag gggctactt 750
 ctcccctccc tcggttccag tctcccttt aaaagcctgt ggcattttc 800
 ctccccctcc ctaactttag aaatgttgta ctggctatt ttgattaggg 850
 aagagggatg tggtctctga tctctgttgt cttctgggt ctgggggtt 900
 gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
 ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000
 cagctctgag tcttggaaat gttgttaccc ttggaagata aagctgggtc 1050
 ttcaggaact cagtgtctgg gagaaagca tggccagca ttcatgtgt 1100
 gttcctttct gcagtggttc ttatcaccac ctccctccca gccccggcgc 1150
 ctcagccccca gccccagctc cagccctgag gacagctctg atggagagc 1200
 tggggcccccct gagcccactg ggtcttcagg gtgcactgga agctgggtt 1250
 cgctgtcccc tgcacttc tcgcactggg gcatggagtg cccatgcata 1300
 ctctgctgcc ggtccccctca cctgcacttg aggggtctgg gcagtccctc 1350
 ctctccccag tgtccacagt cactgagcca gacggtcggt tggAACATGA 1400
 gactcgaggc tgagcgtgga tctgaacacc acagccccctg tactgggtt 1450
 gcctcttgtc cctgaacttc gtttaccag tgcattggaga gaaaattttg 1500
 tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattt 1550
 ttttatttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155					160					165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
				170					175					180

Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
agttcatagg gtcctgggtc cccgaaccag gaagggttga gggAACACAA 100
tctgcaagcc cccgcgaccc aagtgggggg ccccggtttg gggtcctccc 150
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<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
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20 25 30
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly
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Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala
				65					70				75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys
				80					85				90	
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg
				95					100				105	
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr
				110					115				120	
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu
				125					130				135	
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg
				140					145				150	
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu
				155					160				165	
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly
				170					175				180	
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys
				185					190				195	
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln
				200					205				210	
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu
				215					220				225	
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys
				230					235				240	
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val
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Cys Gln Lys Ile

<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens

<400> 71
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ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
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Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30
Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
245 250 255

Val Gln Asn Ser Thr Tyr Thr Ser Val Ile Thr Ser Cys Ser
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
305 310 315

Gly His Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
320 325 330

Ser Ser Lys Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
350 355 360

Leu Ile Arg

<210> 73
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 73
aattcatggc aaatatttcc cttccc 26

<210> 74
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 74
tggtaaactg gcccaaactc gg 22

<210> 75
<211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcat ccgtccttgg ctcaggattt ggagagctt caccaccaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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ccactctcag caccccacat ttgcatctgc tggtgacact gccaccatca 1950
caataaagtc cccatctgat tttaaaaaaaaaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu
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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
														30

Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
														45

Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
														60

Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
														75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90
 Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105
 Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
 110 115 120
 Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
 125 130 135
 Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
 140 145 150
 Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
 155 160 165
 Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu
 170 175 180
 His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
 185 190 195
 Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
 200 205 210
 Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
 215 220 225
 Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
 230 235 240
 Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
 245 250 255
 Val Thr Val Leu Leu Ala Ala Arg Arg Arg Gly Gly Tyr Glu
 260 265 270
 Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
 275 280 285
 Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300
 Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315
 Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330
 Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
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Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45

Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60

Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75

Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90

Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
 110 115 120
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
 125 130 135
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
 140 145 150
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
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 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
 170 175 180
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
 185 190 195
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
 200 205 210
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
 215 220 225
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
 230 235 240
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
 245 250 255
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
 260 265 270
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
 275 280 285
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
 290 295 300
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
 305 310 315
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
 320 325 330
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
 335 340 345
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
 350 355 360
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
 365 370 375
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
 380 385 390
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser		
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
470	475	

<210> 80

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 80

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<210> 81

<211> 23

<212> DNA

<213> Homo sapiens

<220>

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<400> 81

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<210> 82

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-49

<223> Synthetic construct.

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<210> 83

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

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gccaaagggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84

<211> 567

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu
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Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln
														30
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu
														45
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln
														60
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala
														75
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala
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Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn
														105
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser
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His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu
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Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His
														150
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys
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155									160					

Leu	Gly	Tyr	Ala	Leu	Arg	Pro	Gln	Glu	Lys	Gly	His	Ser	Pro	Glu
				170				175						180
Asp	Ile	Tyr	Gln	Met	Ala	Leu	Asn	Gln	Ala	Leu	Lys	Asp	Leu	Lys
				185				190						195
Ala	Leu	Gly	Cys	Arg	Lys	Ala	Met	Lys	Lys	Phe	Glu	Arg	His	Thr
				200				205						210
Leu	Leu	Glu	Tyr	Leu	Leu	Gly	Glu	Gly	Asn	Leu	Ser	Arg	Pro	Ala
				215				220						225
Val	Gln	Leu	Leu	Gly	Asp	Val	Met	Ser	Glu	Asp	Gly	Phe	Phe	Tyr
				230				235						240
Leu	Ser	Phe	Ala	Glu	Ala	Leu	Arg	Ala	His	Ser	Cys	Leu	Ser	Asp
				245				250						255
Arg	Leu	Gln	Tyr	Ser	Arg	Ile	Val	Gly	Gly	Trp	Asp	Leu	Leu	Pro
				260				265						270
Arg	Ala	Leu	Leu	Ser	Ser	Leu	Ser	Gly	Leu	Val	Leu	Leu	Asn	Ala
				275				280						285
Pro	Val	Val	Ala	Met	Thr	Gln	Gly	Pro	His	Asp	Val	His	Val	Gln
				290				295						300
Ile	Glu	Thr	Ser	Pro	Pro	Ala	Arg	Asn	Leu	Lys	Val	Leu	Lys	Ala
				305				310						315
Asp	Val	Val	Leu	Leu	Thr	Ala	Ser	Gly	Pro	Ala	Val	Lys	Arg	Ile
				320				325						330
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Arg	His	Met	Gln	Glu	Ala	Leu	Arg
				335				340						345
Arg	Leu	His	Tyr	Val	Pro	Ala	Thr	Lys	Val	Phe	Leu	Ser	Phe	Arg
				350				355						360
Arg	Pro	Phe	Trp	Arg	Glu	Glu	His	Ile	Glu	Gly	Gly	His	Ser	Asn
				365				370						375
Thr	Asp	Arg	Pro	Ser	Arg	Met	Ile	Phe	Tyr	Pro	Pro	Pro	Arg	Glu
				380				385						390
Gly	Ala	Leu	Leu	Leu	Ala	Ser	Tyr	Thr	Trp	Ser	Asp	Ala	Ala	Ala
				395				400						405
Ala	Phe	Ala	Gly	Leu	Ser	Arg	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Leu
				410				415						420
Asp	Asp	Val	Ala	Ala	Leu	His	Gly	Pro	Val	Val	Arg	Gln	Leu	Trp
				425				430						435
Asp	Gly	Thr	Gly	Val	Val	Lys	Arg	Trp	Ala	Glu	Asp	Gln	His	Ser
				440				445						450
Gln	Gly	Gly	Phe	Val	Val	Gln	Pro	Pro	Ala	Leu	Trp	Gln	Thr	Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
<211> 3316
<212> DNA
<213> Homo sapiens

<400> 85
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gaactcagag ccggaaagcc cccattcaact agaagcactg agagatgcgg 200
ccccctcgca gggctgaat ttccctgctgc tgttcacaaa gatgttttt 250
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cctgacattt ggagctgcca tcttcttgc gctgatcacc agaccta 350
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ggagcacgga agggggtttc ccagaagaac aatgacctaa caagttgctg 450
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<210> 86
<211> 739
<212> PRT
<213> Homo sapiens

<400> 86
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Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile
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Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys
					65				70			75		
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg
					80				85			90		
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val
					95				100			105		
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn
					110				115			120		
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu
					125				130			135		
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu
					140				145			150		
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys
					155				160			165		
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His
					170				175			180		
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala
					185				190			195		
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr
					200				205			210		
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu
					215				220			225		
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile
					230				235			240		
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu
					245				250			255		
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro
					260				265			270		
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu
					275				280			285		
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe
					290				295			300		
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys
					305				310			315		
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr

	320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val			
335	340	345	
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr			
350	355	360	
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val			
365	370	375	
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg			
380	385	390	
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro			
395	400	405	
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn			
410	415	420	
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val			
425	430	435	
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp			
440	445	450	
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu			
455	460	465	
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser			
470	475	480	
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val			
485	490	495	
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe			
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Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu			
515	520	525	
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr			
530	535	540	
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn			
545	550	555	
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala			
560	565	570	
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp			
575	580	585	
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile			
590	595	600	
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu			
605	610	615	

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
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Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635				640					645	
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650				655					660	
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
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Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680				685					690	
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695				700					705	
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710				715					720	
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
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His	Ile	Gln	Asp											

Homo sapiens

<210>	87				
<211>	2725				
<212>	DNA				
<213>	Homo sapiens				
<400>	87				
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ccaggacatt	gtgtacccgc	caatccgta	tggacgactg	gaagcccagc	150
cccctcatca	agccctttgg	ggctcgaaag	aagcggagct	ggtaccttac	200
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cagggccgt	gctttcctg	ctggtgactg	tcattgtcaa	tatcaagttg	300
atcctggaca	ctcggcgagc	catcagtgaa	gccaatgaag	acccagagcc	350
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gccacagtat	ggcaaaacgt	gtgtttgaca	cgtactcacc	tcatgaggat	600
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aaaaaaaaaaaa aaaaaaaaaaa aaaaa 2725

<210> 88
<211> 660
<212> PRT
<213> Homo sapiens

<400> 88
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Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
35 40 45
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
50 55 60
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65 70 75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
80 85 90
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
95 100 105
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
110 115 120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
140 145 150

Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
155 160 165

Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
170 175 180

Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
185 190 195

Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
200 205 210

Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
215 220 225

Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
230 235 240

Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
245 250 255

Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
260 265 270

Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
275 280 285

Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
290 295 300

Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
305 310 315

Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
320 325 330

Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
335 340 345

Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
350 355 360

Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
365 370 375

Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
380 385 390

Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
395 400 405

Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
410 415 420

Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu		
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr		
650	655	660

<210> 89
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgttg acacg 25
<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22
<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtac aggc 24
<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26
<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacacctat gaggatgagg ccatggtgct attcctcaac atggtag 47
<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94

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actgaaATT tggTGTCTAG tggttgTGGG tgaataaAGG agggcagaAT 150
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggTggat 200
gttacgtggc cggaatcatt cccttggctg ttaatttctc agagGAACGA 250
ctgaagctgg tgactgtttt gggtgctggc cttctctgtg gaactgctct 300
ggcagtcATC gtgcctgaag gagtACATGC cctttatgaa gatattcttG 350
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aaAGCAGCAG aaaaatcagt tgtccatgaa catgAGCACA gCcACGACCA 450
cacacAGCTG catgcctata ttggTgtttc cctcgTTCTG ggcttcgttt 500
tcATGTTGCT ggtggaccAG attggtaACT cccatgtgca ttctactgac 550
gatccagaAG cagcaaggTC tagcaattcc aaaatcacca ccacgctggg 600
tctggTTGTC catgctgcAG ctgatggTgt tgctttggA gcAGcAGcAT 650
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cttagAGCGG aatcgaatca gaaAGCactt gctggTcttt gcattggcag 800
caccAGTTat gtccatggTG acataacttag gactgagtaa gagcAGtaAA 850
gaAGCCCTT cagaggtgaa cGCCAcGGGA gtggccatgc ttttctctgc 900
cgggacattt ctTTatgttG ccacagtaca tgcctccct gaggtggcgc 950
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ttgtcaaata aatagcagat ttagtgtca aaaaaaa 3037

<210> 95
<211> 307
<212> PRT
<213> Homo sapiens

<400> 95
Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu
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Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe
20 25 30
Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
65 70 75
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90
Val Val His Glu His Ser His Asp His Thr Gln Leu His
95 100 105
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu		
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile		
290	295	300
Leu Ser Val Gly His Gln His		
305		

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 cttgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctccattha gcctgctgtc tctggctatg ttgggtggat 50

<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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gcccccggatc cccgagtggc ggccggagcc tcgaaaagag atttcagcg 100
ctgattttga gatgatgggc ttggaaacg ggcgtcgca catgaagtcg 150
ccgccccctcg tgctggccgc cctggtggcc tgcatacatcg tcttggctt 200
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250
tggagctgga aggcagggtc cgcaaggcgg ctgcagagag aggccgcgtg 300
gagctgaaga agaaccgagtt ccagggagag ctggagaagc agcgggagca 350
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
agctgtacca ggacgaaaag gcgggtttgg tgaataacat caccacaggt 450
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ggaatcatac actctgaatt gaactggaat cacatatttc acaacaggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400

gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr
 245 250 255
 Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu
 260 265 270
 Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val
 275 280 285
 Gly Gly Arg Gly Phe Gly Ala Gly Glu Leu Gly Gln Thr Pro
 290 295 300
 Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met
 305 310 315
 Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu
 320 325 330
 Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu
 335 340 345
 Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser
 350 355 360
 Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile
 365 370 375
 Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu
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 395 400
 <210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens
 <400> 101
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tgtatagccc cacagcagtc ttccccagca ccccaccaga ggagccagag 950
gtgattcctc aagttagcct tgtgccacg ctggccctgc tgctggcct 1000
gcccatccca tttgggaata tcgggaaagt gatggctgag ctattctcag 1050
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gctagctggg cttttcatac gttgccctga agagacacct gtttgccact 1950

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agtgtataaa aatgataata t 3671

<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe
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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu
					20				25				30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
					35				40				45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50				55				60		
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
					65				70				75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
					80				85				90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
					95				100				105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
					110				115				120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
					125				130				135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
					140				145				150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
					155				160				165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
					170				175				180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
					185				190				195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp		
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys		
230	235	240
His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met		
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr		
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp		
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu		
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro		
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu		
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala		
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala		
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser		
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala		
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala		
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr		
410	415	420
Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala		
425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg		
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys		
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys		
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile		
485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Phe
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
635 640 645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
650 655 660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg	Gly
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala	Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val Thr	Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln Pro	Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp	Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly	Ala Val Ser Ser Trp Phe	
1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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gcagttccct gtgtctctgg tggtttgcct aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tggtaatac 350
taaatcaaac agaacgtggt cccagtgtgt gaccaaccac acgctgggtc 400
tcacacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgtttgcc catatctatt accgtgtttc tttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattctt gtgcctgctg 700
aaaaaaatcgt gattaactt atcaccctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagccca gcgggaacct gaggccccct caggaggaag 850
aggaggtgaa acattnaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtccct 950
cagcagaaca ataccccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcacggtt 1100
ggcagtcctg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccccctggcg caggagcaca cagactcgga ggagggccg 1200
gaggaagagc catcgacgac cctggtcgac tggatcccc aaactggcag 1250

gctgtgtatt ctttcgtgtt ccagctcga ccaggattca gagggctgcg 1300
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 cgtgtgtat tggttcatgc atgttaggtct cttaacaatg atggtgggcc 1650
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 aaatgttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20				25					30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35				40					45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50				55					60	
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65				70					75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80				85					90	
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95				100					105	
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110				115					120	
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125				130					135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140				145					150	
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155				160					165	

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile
				170					175				180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys
				185					190				195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys
				200					205				210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val
				215					220				225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro
				230					235				240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu
				245					250				255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser
				260					265				270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys
				275					280				285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys
				290					295				300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Val	Ser	
				305					310				315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu
				320					325				330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp
				335					340				345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro
				350					355				360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr
				365					370				375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser
				380					385				390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly
				395					400				405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro
				410					415				420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly
				425					430				435	
Leu	Tyr	Val	Gln	Met	Glu	Asn								
				440										

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcggtgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgt cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

cggacgcgtg ggccggacgcg tggggcggacg cgtgggtctc tgccccggaga 50

cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100

tctgctgact gtggccaccg ccctgatgct gcccgtaag ccccccgcag 150

gctcctgggg ggcccagatc atcgggggccc acgaggtgac ccccccactcc 200

aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250

cttcctgctg cgagcccgct gggtggtctc ggccgcccac tgcttcagcc 300

acagagacct ccgcactggc ctggtggtgc tgggcgcccac cgtcctgagt 350

actgcggaggc ccacccagca ggtgtttggc atcgatgctc tcaccacgca 400

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gggagaaggg ccaggccccc cacagcgggg acacggtgcc gggtggtgg 550

ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600

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ccccaggaga agccgcctga gccacaaacct tgcggcatgc aaatgagatg 950

gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000

tgttcagggt tggggtgaaa cgggcagcgg tggggcacac ccattccaca 1050

tgcaaaggc agaagcaaac ccagtaaaat gtttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
1 5 10 15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagtcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
gagctaccca ggccgttgt gtgcagcaag ctccgcgccg actccggacg 50
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cgctgtcggc gctgggcacg gtagcaggcg ccgcccgtgt gctcaaggac 150
tatgtcaccg gtggggcttg cccccagcaag gccaccatcc ctggaaagac 200

ggtcatcggtg acgggcgcca acacaggcat cgaaaagcag accgccttgg 250
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
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aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
gatcagttt ggcgttaacc acctgggtca ctttcttgc acaaacttgc 550
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gagagcaggt gcaggtgtca tcccgagttc aggctctgca cggcatggag 1700
tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
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<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala
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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys
			20				25						30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly
				35				40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg
					50			55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys
			65				70					75		
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His
				80			85					90		
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg
				95				100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110				115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr
				125				130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His
				140				145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155				160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly
				170				175					180	
His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				185				190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200				205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215				220					225	

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
230 235 240

Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro
245 250 255

Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro
260 265 270

Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly
275 280 285

Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala
290 295 300

Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg
305 310 315

Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro
320 325 330

Arg

<210> 117
<211> 2249
<212> DNA
<213> Homo sapiens

<400> 117
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gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgccc 150
agcgcggct gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200
cggctgcggg acctgactag attctacgac aaggtacttt ctttgcattga 250
ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
gagaacatcc gagctctgaa ggatggctat gagaagggtgg agcaagac 400
tccagccctt gaggaccttg agggagcagc aaggccctg atgcggctgc 450
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cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtggtgcc 1150
atcaggggag aagcagttac aagtggagta ccgcattcagc aaaagtgcct 1200
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ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
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cttgaccaca gggaccaaga agtggcaatg aggacacctg caggagggc 2050
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agcccaagca gggagtgcc ccctccca gacatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
 245 250 255
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
 260 265 270
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
 275 280 285
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
 290 295 300
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
 305 310 315
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
 320 325 330
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
 335 340 345
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
 350 355 360
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
 365 370 375
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
 380 385 390
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
 395 400 405
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
 410 415 420
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
 425 430 435
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
 440 445 450
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
 455 460 465
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
 470 475 480
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
 485 490 495
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
 500 505 510
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
 515 520 525
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

530

535

540

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcatgggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
gagatagggta gtctgggttt aagttcctgc tccatctca gggccctgc 50
tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
gaatcgcccc tggcaggtgg ggccacgagc gctggctgag ggacccgagcc 150
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgcc 200

cgccgggact cgagcagggt gcgcactgc gcgcgttct cctacctctg 250
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
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aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcacccctc 400
gggcgtcgtc atgttcatgg tctccttcat tggtgtgctg gcgtccctcc 450
gtgacaacct gtaccccttc caagcattca tgtacatcct tggatctgc 500
ctcatcatgg agctcattgg tggcgtggtg gccttgacct tccggaacca 550
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tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttcccccgc 1700
gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750
catgtttgt tttgtttta aaaaaaaaa 1778

<210> 123
<211> 294
<212> PRT
<213> Homo sapiens

<400> 123
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Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
20 25 30
Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
35 40 45
Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
50 55 60
Ala Pro Ala Ile Ile Leu Ile Leu Gly Val Val Met Phe Met
65 70 75
Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
80 85 90
Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
95 100 105
Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
110 115 120
Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
125 130 135
Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
140 145 150
Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
155 160 165
Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
170 175 180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
185 190 195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
200 205 210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
215 220 225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

	230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val		Leu Leu Thr Leu Leu Tyr	
245		250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp		
260	265		270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly		
275	280		285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn			
290			

<210> 124
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 124
atcatctatt ccaccgtgtt ctggc 25

<210> 125
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 125
gacagagtgc tccatgatga tgtcc 25

<210> 126
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 126
cctgtctgtg ggcatctatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127
<211> 1636
<212> DNA
<213> Homo sapiens

<400> 127

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ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcacac 150
tgcagttctc atcctcgccc caaaagtcat caaagaaaaag ctgacacagg 200
agctgaagga ccacaacgccc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggc atcacagcta 350
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cctctctgca atcaataaac acttgccgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
			20					25				30		
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
				35				40				45		
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50				55				60		
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65				70				75		
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80				85				90		
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95				100				105		
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110				115				120		
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125				130				135		
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140				145				150		
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155				160				165		
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
				170				175				180		
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185				190				195		
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200				205				210		
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215				220				225		

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
 230 235 240
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
 245 250 255
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
 260 265 270
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
 275 280 285
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
 290 295 300
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
 305 310 315
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
 320 325 330
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
 335 340 345
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
 350 355 360
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
 365 370 375
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
 380 385 390
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
 395 400 405
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
 410 415 420
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
 425 430 435
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
 440 445 450
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
 455 460 465
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480
 Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
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ctaacaaaag acctgtaata agaatgaatg gagacaagtt ccgtcgccctt 200
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ttttagctg aaacacacat tggcttctg tt当地atggt gaggatctt 850
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aaaaaaaaaa aaa 2213

<210> 130
<211> 335
<212> PRT
<213> Homo sapiens

<400> 130
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Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
35 40 45

Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
50 55 60

Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
65 70 75

Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
80 85 90

Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp
				110					115					120
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser
				125				130						135
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg
				140					145					150
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln
				155				160						165
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val
				170				175						180
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu
				185				190						195
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met
				200				205						210
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys
				215				220						225
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg
				230				235						240
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn
				245				250						255
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His
				260				265						270
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu
				275				280						285
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys
				290				295						300
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser
				305				310						315
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr
				320				325						330
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				335										

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
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<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

<400> 132
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Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly
			80					85				90		
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu
			95			100			100			105		
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly
			110			115			115			120		
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His
			125			130			130			135		
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala
			140			145			145			150		
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg
			155			160			160			165		
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr
			170			175			175			180		
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr
			185			190			190			195		
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr
			200			205			205			210		
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His
			215			220			220			225		
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys
			230			235			235			240		
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr
			245			250			250			255		
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys
			260			265			265			270		
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu
			275			280			280			285		
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu
			290			295			295			300		
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly
			305			310			310			315		
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr
			320			325			325			330		
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile
			335			340			340			345		
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile
			350			355			355			360		
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys 380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser 395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg 410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile 425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr 440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln 455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val 470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile 485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln 500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln 515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val 530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

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Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
35 40 45

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala		
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile		
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr		
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala		
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro		
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro		
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr		
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile		
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr		
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg		
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser		
215	220	225
Leu Thr Gly Tyr Val		
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<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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agggtgtggag acaagatcta caaccccttg gagcagtgtct gttacaatga 200
cgccatcggt tccctgagcg agaccggcca atgtggtccc ccctgcaccc 250
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aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
agctccaagc cattgttatgg cccatgtggg agactgatgg gacatggaga 550
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acctgtaaaa 610

<210> 136

<211> 119

<212> PRT

<213> Homo sapiens

<400> 136

Met	Val	Pro	Arg	Ile	Phe	Ala	Pro	Ala	Tyr	Val	Ser	Val	Cys	Leu
1				5					10				15	
Leu	Leu	Leu	Cys	Pro	Arg	Glu	Val	Ile	Ala	Pro	Ala	Gly	Ser	Glu
			20					25					30	
Pro	Trp	Leu	Cys	Gln	Pro	Ala	Pro	Arg	Cys	Gly	Asp	Lys	Ile	Tyr
			35					40					45	
Asn	Pro	Leu	Glu	Gln	Cys	Cys	Tyr	Asn	Asp	Ala	Ile	Val	Ser	Leu
			50					55					60	
Ser	Glu	Thr	Arg	Gln	Cys	Gly	Pro	Pro	Cys	Thr	Phe	Trp	Pro	Cys
			65					70					75	
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80					85					90	
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
			95					100					105	
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
					110				115					

<210> 137

<211> 771

<212> DNA

<213> Homo sapiens

<400> 137

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gtggggacaa gttctacgac cccctgcagc actgttgcta tggatgatgcc 200
gtcgtgcccct tggccaggac ccagacgtgt ggaaactgca ctttcagagt 250

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gctgtttgggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
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ccttcataaa ttctggacag catgagatgc gtgtgctgtat gggggccca 600
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accccaaggc tggctgggaa acccttcacc cttctgtgag atttccatc 700
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tatgtacttt ataaatgaaa a 771

<210> 138
<211> 110
<212> PRT
<213> Homo sapiens.

<400> 138
Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
1 5 10 15
Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
20 25 30
Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45
Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60
Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75
Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
.80 85 90
Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105
Cys Arg Ser Val Ser
110

<210> 139
<211> 2044
<212> DNA
<213> Homo sapiens

<400> 139

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ctcccccggca ccagaagttc ctctgcgcgt ccgacggcga catggcgctc 150
cccacggccc tggaggccgg cagctggcgc tggggatccc tgctttcgc 200
tctcttcctg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250
cgccgtattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300
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gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
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caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
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gggaaggtga gtggagaggg gcacctgccc cccgcctcc ccatcccc 1900
ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
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Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
20 25 30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
35 40 45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
50 55 60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
65 70 75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
80 85 90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
95 100 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
110 115 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
125 130 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141
<211> 1732
<212> DNA
<213> Homo sapiens

<400> 141
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cttagacctc ctttcctgcc ctcccttcct gccaccgct gttcctggc 150
ccttctccga ccccgctcta gcagcagacc tcctgggtc tgtgggttga 200
tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cttcccgact 250
ccgctcccg accagcggcc tgaccctgg gaaaggatgg ttcccgaggt 300
gagggtcctc tcctccttgc tggactcgc gctgctctgg ttccccctgg 350
actcccacgc tcgagcccgcc agacatgt tctgcctttt ccatggaaag 400
agatactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccattgag ctgttccccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cgatgaaaga ggacagtgtg 850
cagtcgctcc atgggggtgag acatcctcag gatccatgtt ccagtgtgc 900
tgggagaaaag agaggccccgg gcaccccccagc ccccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggccagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcattgg 1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggcccccatt gccctgcattt ctagcacct gtgaggatgg ccggcaggac 1150
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agtggctggg aagtgtgc a agatttgc ccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
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cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga gaaaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcaact ggaacgttcc cctagcccaag accctggagc tgaaggtcac 1600
ggccagtcac gacaaagtga ccaagacata acaaagacct aacagttgc 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
 1 5 10 15
 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
 20 25 30
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120
 Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
 125 130 135
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
 140 145 150
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
 155 160 165
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
 170 175 180
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
 185 190 195
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
 200 205 210
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
 215 220 225
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
 230 235 240
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
 245 250 255
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
 260 265 270
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
 275 280 285
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450
Thr		
<210> 143		
<211> 693		
<212> DNA		
<213> Homo sapiens		
<400> 143		
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cttgcggaaa atgctgatct cagtcgaat gctggcgca gggctggcg 150		
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cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350		
ggcggccagcg ggaggtcacc gtgagaccgg acttgcctcc gtggcgccg 400		
gaccttggct tggcgcagg aatccgaggc agcctttctc cttcgtggc 450		

ccagcggaga gtccggacccg agataccatg ccaggactct ccggggtcct 500
gtgagctgcc gtcgggtgag cacgttccc ccaaaccctg gactgactgc 550
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aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaaaaaaaa 650
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 693

<210> 144
<211> 93
<212> PRT
<213> Homo sapiens

<400> 144
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
1 5 10 15
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
20 25 30
Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
35 40 45
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
50 55 60
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
65 70 75
Trp Arg Lys Asr Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
80 85 90
Arg Ser Pro

<210> 145
<211> 1883
<212> DNA
<213> Homo sapiens

<400> 145
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caggctgcca tggggcccaag caccctctc ctcatcttgt tcctttgtc 150
atggtcggga cccctccaag gacagcagca ccaccttgg gagtacatgg 200
aacggcact agctgctta gaggaacggc tggcccagtg ccaggaccag 250
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gagaccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagttagatc aatgaagatt 550
ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600
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aaggctttg ggctgtctat gccacccggg aggatgacag gcacttgtgt 1000
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
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tctatgtcgt ctataacacc cgtcctgcca gtcgggcccc catccagtgc 1150
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gagatgagga agaaagagga ggaggttga ggagctagcc ttgtttttg 1350
catotttctc actcccatac atttatatta tatccccact aaatttctt 1400
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acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750
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gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212>. PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270

Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285

Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300

Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315

Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330

Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
335 340 345

Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360

Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375

Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390

Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 147
gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50
ccgctcacgc agaggctctc cgtggcttcc gcacccctgag cattaggcca 100
gttctccctct tctctcta at ccatccgtca cctctccctgt catccgtttc 150
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
ttgggtctga gtctcctcaa gctggatca gggcagtggc aggtgtttgg 250
gccagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctcct 300
gtttccctgtc tcctaagacc aatgcagagg ccatggaagt gcgggttc 350
agggggccagt tctctagcgt ggtccaccc tacagggacg ggaaggacca 400
gccatattatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
attctattgc ggagggccgc atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
gaaggccatc tggagctac aggtgtcagc actgggctca gttcctctca 600
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
tcgggcttgt tccccggcc cacagcgaag tggaaaggcacaaggaca 700
ggatttgcac acagactcca ggacaaacag agacatgcat ggcctgttg 750
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tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850
aggagatacc ttttcgagc ctatatcgta gcacctggct accaaagtac 900
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ttcttctcca aattccagtg gaaaatccag gcggaaactgg actggagaag 1000
aaagcacgga cagggcagaat tgagagacgc ccggaaacac gcagtggagg 1050
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aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
gagatttaca aggaagagtg tggggcttc tcagagttc caagcaggga 1200
aacattactg ggaggtggac ggaggacaca ataaaaggta ggcgtggga 1250
gtgtgccggg atgatgtgga caggaggaag gagtagtga ctttgcctcc 1300
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
cattaaatcc ccgtttatc agcgtttcc ccaggacccc acctacaaaa 1400
ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
aaatgaccag tcccttattt ataccctgac atgtcggtt gaaggcttat 1500
tgaggcccta cattgagttat ccgtcctata atgagcaaaa tggaactccc 1550
atagtcatct gcccagtac ccaggaatca gagaaagagg cctctggca 1600
aaggccctct gcaatcccag agacaagcaa cagttagtcc tcctcacagg 1650
caaccacgccc cttccctcccc aggggtgaaa tgttaggatga atcacatccc 1700
acattcttct ttagggatataaggatctct ctcctcagatc caaagtcccg 1750
cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac 1800
atgggagtca ggtgtcatgg ctgcctgag ctgggaggga agaaggctga 1850
cattacattt agtttgctct cactccatct ggctaagtga tcttgaata 1900
ccacctctca ggtgaagaac cgtaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgtt tcctaattgtt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
1 5 10 15
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys Gly	Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val Thr	Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Gln Ala	Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgctgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc a cagtatcaag gcaggacaaa actggtaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcgccg gcggttgcgg aggcttcctt 50
ggtcggattt caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc ggcgcatttag gaggctggcg agcctggcg 150
gcctcgccct gttgtgtgc gcccggccg ccggccgcgt cgccctcagcc 200
gcctcgccg ggaatgtcac cggtgccggc gggccgcgg ggcagggtgaa 250
cgcgatcgccg ggccccgggt tgccccggcga gcccagccac ccctcccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350
accgtccacc gacccctggc tgcgacttct ccagcccaat ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcgcccc ctcgccgacc acccctccgg cgccggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgccgg accaccctt cgacgaccac 550
tggcccgcgccg ccgaccaccc ctgttagcgac caccgtaccg gcgcccacga 600
ctccccggac cccgacccccc gatctcccca gcagcagcaa cagcagcgtc 650
ctccccaccc cacctgcoac cgaggccccc tcttcgcctc ctccagagta 700
tgtatgtaac tgctctgtgg ttggaagcct gaatgtaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcgccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggtt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgttagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga gggtggaaact gaagtttatt ttatTTAGC aaggaaaaaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacaaggaggatga 1000
gggtcataga tttacaaaat attttatata cttttattct cttaactttat 1050
atgttatatt taatgtcagg attaaaaaac atctaattta ctgatTTAGT 1100
tcttcaaaag cactagagtc gccaattttt ctctggata atttctgtaa 1150
atttcatggg aaaaaattat tgaagaataa atctgcttc tggaagggt 1200
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250
atataccatt ggagtttag gaaatttgtt gtttggtta ttttctc 1300
taatcaaaaat tctacatttg tttcttgga catctaaagc ttaacctggg 1350
ggtaccctaa tttatTTAAC tagtgtaag tagactggtt ttactctatt 1400
taccagtaca ttttgagac caaaagtaga ttaagcagga attatctta 1450
aactattatg ttatTTGGAG gtaatttaat ctgtggaaat aatgtactgt 1500
tatctaagca tttgcTTGT actgcactga aagtaattat tctttgaccc 1550
tatgtgaggc acttggcttt ttgtggaccc caagtcaaaa aactgaagag 1600
acagtattaa ataatgaaaa aaataatgac aggttataact cagtgtaaacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttggca 1700
agtaatttcc tttcactgag cttgtttctt ctcaagggtt tggtgaagat 1750
taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
ctggTTTGTt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgtttaaga acttttagct ccttgacaaa gaagtgcctt atactttagc 1900
actaaatatt ttaaatgctt tataaatgat attatactgt tatggaatat 1950
tgtatcatat tgtatgttat taaaaatgta gaagaggctg ggccgggtgg 2000
ctcacgcctg taatcctagc actttggag gccaaaggcggtgg 2050
tgaggccagg agttcttagat gagcctggcc agcacagtga aaccccggtct 2100
ctactaaaaa tacaaacaaa ttagctggc gtggtggcac acacctgttag 2150
tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtag 2250
agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
1 5 10 15

Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
20 25 30

Val Thr Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
80 85 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
110 115 120

Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
125 130 135

Thr Thr Leu Ser Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
155 160 165

Asp Leu Pro Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

170	175	180
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro	Glu Tyr Val Cys Asn	
185	190	195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr		
200	205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys		
215	220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu		
230	235	240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro		
245	250	255

Cys Asn Arg

```

<210> 154
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 154
     aactgctctg tggttggaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 155
     cagtacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-38
<223> Synthetic construct.

<400> 156
     agtttatcag gggcttcact gtgaaacctg caaagagg 38

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<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100
ctggaccctg agcagcttct tggccctgg tacgtgcttgc cggtggcctc 150
ccggggaaaag ggctttgccca tggagaagga catgaagaac gtcgtgggggg 200
tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
ctccggatgg gtgtttgaga atccctcaat aggcggtgtg gagctctggg 350
tgctggccac caacttcaga gactatgcca tcatacgttac tcagctggag 400
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
agccagccag gaggccatgg ggctcttac caagtggagc aggagcctgg 500
gcttcctgtc acagtagcag gcccagctgc agaaggacct cacctgtgct 550
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcccaca 600
gggtcctgtg acctcggcca gtgtccaccc acctcgctca gcggctcccg 650
gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
<211> 163
<212> PRT
<213> Homo sapiens

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
1 5 10 15
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
20 25 30
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
35 40 45
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
50 55 60
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
65 70 75
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

aacagacgtt ccctcgccgc cctggcacct ctaaccccaag acatgctgct 50
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100
gtaaaactgct gacgatgcag agttccgtga cggtgcagga aggctgtgt 150
gtccatgtgc cctgctcctt ctcctacccc tcgcatggct ggatttaccc 200
tggccccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct cttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcc aagaaggatgtga tgcggggaga tacttcttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctcccccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacacccct atgatctctt ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcaccc tcatcccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttggaaat ggctcatctc tgtcaactccc agagggccag tctctgcgcc 850
tggctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

ggtgctggag ctgccttggg tgcacctgag gcatgcagct gaattcacct 1000
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050
ctgcagagca aagccacatc aggagtact cagggggtgg tcgggggagc 1100
tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcggttag 1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
acgggcatag agatgcata cgctgtcagg ggttcagcct ctcagggcc 1250
cctgactgaa cttggggcag aagacagtcc cccagaccag cctccccag 1300
cttctgcccgc ctcctcagtg ggggaaggag agtccagta tgcattccctc 1350
agcttccaga tggtaagcc ttggactcg cggggacagg aggccactga 1400
caccgagtagc tcggagatca agatccacag atgagaaact gcagagactc 1450
accctgattt agggatcaca gcccctccag gcaaggagaa agtcagaggc 1500
tgattcttgt agaattaaca gccctcaacg tcatgagcta tgataacact 1550
atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttattttt taactaaaag 1650
acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
1 5 10 15

Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
20 25 30

Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
35 40 45

Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
50 55 60

Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
65 70 75

Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
80 85 90

Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
95 100 105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420

Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
425 430 435

Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450

Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> 161

<211> 739

<212> DNA

<213> Homo sapiens

<400> 161

gacgcccaagt gacctgccga ggtcgccagc acagagctct ggagatgaag 50

accctgttcc tgggtgtcac gctcgccctg gccgctgccc tgtccttcac 100

cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150

tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200

aaggtgacag ccctgggcgg tggaaagttg gaagccacgt tcaccctcat 250

gagggaggat cggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300

agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350

gagctgccc a ggggacca ctacatctt tactgcaaag accagcacca 400

tggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450

accggaggc cctggaagaa tttaagaaat tggtgccagcg caagggactc 500

tcggaggagg acattttcac gcccctgcag acgggaagct gcgttcccga 550

acactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600

acacagagcc cgaccaccc ggacctaccc tccagccatg accctccct 650

gctcccaccc acctgactcc aaataaagtc ctttcccccc aaaaaaaaaa 700

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162

<211> 170

<212> PRT

<213> Homo sapiens

<400> 162

Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15

Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 163
ggagatgaag accctgttcc tg 22

<210> 164
<211> 26
<212> DNA
<213> Artificial .

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 164
ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtcccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtggtt cgggAACGCA gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggcacctg gtacgtgaag gccatggtag tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatac acaggaccc ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagagggtt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgctcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgcccccaga tggctcctga cagcagccca ctgcctcaag 300
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag ccactgagtc ctcccccac cccggcttca 400
acaacagcct ccccaacaaa gaccacccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctggct gtgcgacccc tcaccctctc 500
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gcacgtccag cccccagttt cgcctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgttag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccagggtga ctccgggggc cctctggct gtaaccagtc tcttcaaggc 750
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acaatttagac tggacccacc caccacagcc catcaccctc catttccact 900
tggtgtttgg ttccctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000
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tgtatccccca gccccaaaga cagctcctgg ccatatatca aggttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro
			20					25					30	
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu
			35					40					45	
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala
			50					55					60	
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His
			65				70						75	
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr
			80				85						90	
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys
			95				100						105	
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val
			110				115						120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys
			125				130						135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr
			140				145						150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn
			155				160						165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly
			170				175						180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly
			185				190						195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn
			200				205						210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala
			215				220						225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val
			230				235						240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn					
			245				250							

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
ggctgcggga ctggaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtatgt tgccgggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggtttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaaggctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaaagagg agagcacccga agaagtgaaa atagaagttt tgcatcgtcc 150

agaaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200

atgacggctaa cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaaatgaag gccaccccaa atggttgtt ctgggtgtg ggcaagtcat 300

aaaaggccctaa gacattgctaa tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattt aactttatgc 450
tgtgacaaa ggaccacgga gcattgagac atttaaacaa atagacatgg 500
acaatgacag gcagctctc aaagccgaga taaacctcta cttgcaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
tttagaagat attttaaga agaatgacca tgatggtgat ggcttcattt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcataattgt 700
atttctactt tttttttta gctatttact gtactttatg tataaaacaa 750
agtcactttt ctccaagttt tatttgctat ttttccccta tgagaagata 800
ttttgatctc cccaatacat tgatttttgtt ataataaaatg tgaggctgtt 850
ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900

aaaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15

Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
20 25 30

Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
35 40 45

Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
50 55 60

Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
65 70 75

Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
80 85 90

Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
95 100 105

Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
110 115 120

Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
125 130 135

Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
140 145 150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 183

cctttcagga tgttaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatcctgat atgacttgac acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagagg aagaggagg gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaacccaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
atacttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200
aacgccaggc atgggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
aaggcagggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtgg 350
ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
ctccagcatg gatgacagag caagactccg tctaaaaaag aaaagatagt 500
ttcttgcgttc atttcgcac tgccctctca gtgtttcctg ggatcccctc 550
ccaaataaaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met	Gln	Gly	Pro	Leu	Leu	Leu	Pro	Gly	Leu	Cys	Phe	Leu	Leu	Ser
1				5					10				15	
Leu	Phe	Gly	Ala	Val	Thr	Gln	Lys	Thr	Lys	Thr	Ser	Cys	Ala	Lys
				20				25					30	
Cys	Pro	Pro	Asn	Ala	Ser	Cys	Val	Asn	Asn	Thr	His	Cys	Thr	Cys
				35				40				45		
Asn	His	Gly	Tyr	Thr	Ser	Gly	Ser	Gly	Gln	Lys	Leu	Phe	Thr	Phe
				50				55				60		
Pro	Leu	Glu	Thr	Cys	Asn	Ala	Arg	His	Gly	Gly	Ser	Arg	Leu	
				65				70						

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgc##### aatgcttctt gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttcccca 100
gactttggaa gtgacccacc atggggctca gcatctttt gtcctgtgt 150
gttcttgggc tcagccaggc agccacaccc aagatttca atggcactga 200
gtgtggcgt aactcacagc cgtggcaggt ggggctgtt gagggcacca 250
gcctgcgtg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcaactgca gcggcagcag gtactgggtg cgcctgggg aacacagcct 350
cagccagctc gactggaccc agcagatccg gcacagcggc ttctctgtga 400
cccatcccggtt ctacctggaa gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgccctgtcc cgtccgcgtt accagcagcg ttcaacccct 500
gccccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
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tgcctcaacc tctccatcgt ctcccatgtcc acctgccatg gtgttatcc 650
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atgcctgcca gggtgattct gggggccccc tggtgtgtgg gggagtcctt 750
caaggtctgg tgcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
tcatgaggaa caactgacct gttcctcca cctccacccc cacccctaa 900
cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
ccctagctcc actcttggtg gcctggaaac ttcttggaaac tttaactcct 1000
gccagccctt ctaagaccca cgagcggt gagagaagt tgcaatagtc 1050
tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
<211> 248
<212> PRT
<213> Homo sapiens

<400> 194
Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
1 5 10 15
Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
20 25 30
Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
35 40 45
Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
50 55 60
Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
65 70 75
Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
80 85 90
Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
95 100 105
Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
110 115 120
Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
125 130 135
Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
140 145 150
Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
155 160 165
Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
170 175 180
Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
185 190 195
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

200 205 210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp
215 220 225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp
230 235 240
Ile Arg Met Ile Met Arg Asn Asn
245

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
gcggccacac gcagctagcc ggagcccgga ccaggcgct gtgcctcctc 50
ctcgccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100
tcgcacatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
ggcttgctca aagcccgca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgtatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacactgaa caatgaaggc 300
gagattgacc tgatgtctt aaagaggatg atggagaagc ttgggtgtccc 350
caagacccac ctggagatga agaagatgtat ctcagaggtg acaggagggg 400
tcagtgacac tatatacctac cgagactttg tgaacatgtat gctggggaaa 450
cggtcggctg tcctcaagtt agtcatgtat tttgaaggaa aagccaacga 500
gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
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ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
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gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
1 5 10 15

Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
20 25 30

Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
35 40 45

Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
50 55 60

Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
65 70 75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
110 115 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
125 130 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
140 145 150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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cagcctcctc caggagcgaa gcccgtcaca ccatggcccc cgggtggca 100
gggttcggcg ccgcgcgtgcg cgccgcctg ggcgtggcct tggcgctggc 150
gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200
gctccgctgc cagcgtggac tgccacggc tgggcctccg cgcgttcct 250
cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300
caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350
tgcatctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400
gacctgaagc agcttagagcg actgcgcctg aacaagaata agctgcaagt 450
ccttccagaa ttgctttcc agagcacgccc gaagctcacc agactagatt 500
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acaacaacat cagtcgcata ctggtcacca gctcaacca catgccgaag 700
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<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198
Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
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Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
20 25 30
Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
35 40 45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

Asn	Asn	His	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu
			170				175						180	
Arg	Asp	Leu	Glu	Ile	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Ser	Arg
	185						190					195		
Ile	Leu	Val	Thr	Ser	Phe	Asn	His	Met	Pro	Lys	Ile	Arg	Thr	Leu
	200						205					210		
Arg	Leu	His	Ser	Asn	His	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp
	215						220					225		
Leu	Ser	Asp	Trp	Leu	Arg	Gln	Arg	Arg	Thr	Val	Gly	Gln	Phe	Thr
	230						235					240		
Leu	Cys	Met	Ala	Pro	Val	His	Leu	Arg	Gly	Phe	Asn	Val	Ala	Asp
	245						250					255		
Val	Gln	Lys	Lys	Glu	Tyr	Val	Cys	Pro	Ala	Pro	His	Ser	Glu	Pro
	260						265					270		
Pro	Ser	Cys	Asn	Ala	Asn	Ser	Ile	Ser	Cys	Pro	Ser	Pro	Cys	Thr
	275						280					285		
Cys	Ser	Asn	Asn	Ile	Val	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Met	Glu
	290						295					300		
Ile	Pro	Ala	Asn	Leu	Pro	Glu	Gly	Ile	Val	Glu	Ile	Arg	Leu	Glu
	305						310					315		
Gln	Asn	Ser	Ile	Lys	Ala	Ile	Pro	Ala	Gly	Ala	Phe	Thr	Gln	Tyr
	320						325					330		
Lys	Lys	Leu	Lys	Arg	Ile	Asp	Ile	Ser	Lys	Asn	Gln	Ile	Ser	Asp
	335						340					345		
Ile	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Lys	Ser	Leu	Thr	Ser	Leu
	350						355					360		
Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Ile	Ala	Lys	Gly	Leu	Phe
	365						370					375		
Asp	Gly	Leu	Val	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	Ala	Asn	Lys
	380						385					390		
Ile	Asn	Cys	Leu	Arg	Val	Asn	Thr	Phe	Gln	Asp	Leu	Gln	Asn	Leu
	395						400					405		
Asn	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Lys	Leu	Gln	Thr	Ile	Ser	Lys
	410						415					420		
Gly	Leu	Phe	Ala	Pro	Leu	Gln	Ser	Ile	Gln	Thr	Leu	His	Leu	Ala
	425						430					435		
Gln	Asn	Pro	Phe	Val	Cys	Asp	Cys	His	Leu	Lys	Trp	Leu	Ala	Asp
	440						445					450		
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser

	455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser			
470	475	480	
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe			
485	490	495	
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg			
500	505	510	
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg			
515	520	525	
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn			
530	535	540	
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys			
545	550	555	
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys			
560	565	570	
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu			
575	580	585	
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val			
590	595	600	
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn			
605	610	615	
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser			
620	625	630	
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr			
635	640	645	
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu			
650	655	660	
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly			
665	670	675	
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys			
680	685	690	
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala			
695	700	705	
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln			
710	715	720	
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val			
725	730	735	
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met			
740	745	750	

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr
 755 760 765
 Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile
 770 775 780
 Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe
 785 790 795
 Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg
 800 805 810
 Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu
 815 820 825
 Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu
 830 835 840
 Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly
 845 850 855
 Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu
 860 865 870
 Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser
 875 880 885
 Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr
 890 895 900
 His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala
 905 910 915
 Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
 920 925 930
 Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
 935 940 945
 Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
 950 955 960
 Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
 965 970 975
 His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
 980 985 990
 Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
 995 1000 1005
 Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
 1010 1015 1020
 Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
 1025 1030 1035
 Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggccatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccccgt agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagctc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca gaaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacatttg agggcagaga 550
cctgtccgag tggaaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
ccaggatgct ttgcagcaac gcccctaggat ttgcagtgaa tgtccaaatg 650
cctgtgtcat cttgtcccggt ttcctcccaa tattccttct caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaat 750
gtc 753

<210> 203
<211> 148
<212> PRT
<213> Homo sapiens

<400> 203

Met	Lys	Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr
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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile
		20						25						30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
			35					40						45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
			50					55						60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
			65					70						75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
			80					85						90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
			95					100						105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
			110					115						120
Gln	Gly	Met	Asn	Tyr	Trp	Gln	Gly	Trp	Lys	Lys	His	Cys	Glu	Gly
			125					130						135
Arg	Asp	Leu	Ser	Glu	Trp	Lys	Lys	Gly	Cys	Glu	Val	Ser		
			140					145						

<210> 204
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 204
gcaggcttg aggatgaagg ctgc 24

<210> 205
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 205
ctcattggct gcctggcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctgcagggtt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatcccact gtccttgtt tcggagccag gccacaccgt 50
cctcagcagt gtcatgtgtt aaaaacgccca agctgaatat atcatgcccc 100
tattaaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttaccc ttgtgtctgc ctgtatccca gtgttcaggc tggcttagacg 200
gcggaagaag atcctatattt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaatgtca ccagcttga ctcagttgtt 450
cctgaaaagc tggatgacct agtccccaaag gggaaaaaat tcctgctgct 500
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
ccctagtaca gctgcgtgga agattgacat cccaagattt ggagagggtt 600
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acattatcag gaattgaaga aaatggtcca acagtccgac cttggccagt 700
atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
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gagcctgacc cggtgcaactt ctcagaagca atagaaaagt tcatccgtga 950
accttcctta aaagccacca tgggcctggc tggaaagagcc agagtgaagg 1000
aaaaattttc ccctgaagca tttacagaac agctctaccg atatgttacc 1050
aaactgctgg tataatcaga ttgttttaa gatctccatt aatgtcattt 1100
ttatggattt tagacccagt tttgaaacca aaaaagaaac ctagaatcta 1150
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ctttcctata taccacaccc ccctgtccac ttttcagaaa aaccatgtct 1250
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tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggtttc 1400
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ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
tcactgtcat ctgttaggaa attttgcatt gtcctgtctt tgcctggatc 1550
catagcgaga gtgctctgta ttttttttaa gataatttgc atttttgcac 1600
actgagatataaaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
1 5 10 15

Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
20 25 30

Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
35 40 45

Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
50 55 60

Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
65 70 75

Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
80 85 90

Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
95 100 105

Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
110 115 120

Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
125 130 135

Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
140 145 150

Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
155 160 165

Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
170 175 180

Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
185 190 195

Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
200 205 210

Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
215 220 225

Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
230 235 240

Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
245 250 255

Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
260 265 270

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315
Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
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cttcgcgatc ttccgcgtta ctttcttgct ggcggttgtg ggagccgtgc 100
tctacacctta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaaag 200
tttgcatgag ttccctggta atttgcatga gagatatggg cctgtggtct 250
ccttctggtt tggcaggcgc ctcgtggta gtttggcac tggtatgtta 300
ctgaaggcgc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttatataaggat atcaatctgg tggtggcagt gtgagtgaaa 400
accacatgag gaaaaaaattt tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttt ccctccttcc aaagctttca gaagaattat tagataaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgctt 550
gttttgcata gaagtctgtt acacagatgg taatggtag tacatggaa 600
gatgatcagg aagtcatcg ctccagaag aatcatggca cagttggtc 650
tgagatttggaa aaaggctttc tagatgggtc acttgataaaa aacatgactc 700
ggaaaaaaaca atatgaagat gccctcatgc aactggagtc tgtttaagg 750
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atatttcat 800
tgactcctta gtacaaggaa accttaatga ccaacagatc ctggaaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tgggcaatct gtttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
gccaaactga ctccagttc tgcccagtt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtccttat gcccttggtg 1150
tggtaactca ggatccta atctggccat ctccacacaa gtttgatcca 1200
gatcggttg atgatgaatt agtaatgaaa acttttcct cacttggatt 1250
ctcaggcaca caggagtgtc cagagtttag gtttgcatat atggtagcca 1300
cagtaactct tagtgttattg gtgaagagac tgcacctact ttctgtggag 1350
ggacaggtta ttgaaacaaa gatatgactg gtaacatcat caagggaga 1400
agcttggatc actgtctcaa agagatatta aaattttata cattaaaaat 1450
cattgttaaa ttgattgagg aaaacaacca tttaaaaaaaa atctatgttg 1500
aatccttta taaaccagta tcactttgta atataaacac ctatttgac 1550

ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
1 5 10 15

Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
20 25 30

Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
35 40 45

Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
50 55 60

Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
65 70 75

Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
80 85 90

Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
95 100 105

Ser Leu Leu Arg Tyr Gln Ser Gly Gly Ser Val Ser Glu Asn
110 115 120

His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
125 130 135

Lys Ser Asn Phe Ala Leu Leu Lys Leu Ser Glu Glu Leu Leu

	140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser			
155	160	165	
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val			
170	175	180	
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln			
185	190	195	
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu			
200	205	210	
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu			
215	220	225	
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys			
230	235	240	
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser			
245	250	255	
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser			
260	265	270	
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys			
275	280	285	
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys			
290	295	300	
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val			
305	310	315	
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu			
320	325	330	
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln			
335	340	345	
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg			
350	355	360	
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro			
365	370	375	
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp			
380	385	390	
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly			
395	400	405	
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr			
410	415	420	
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val			
425	430	435	

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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tcagggcttg tgccctctcg ctgcctgacg ctgcctggcgc atctggtggt 150
cgtoatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt cacccccgag gatgtatgaca agcaggacat tcagctggtg 250
gccgcgcgtct ctgtcacccct gggcctcttt gcagtggagc tggccgggtt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcatcc gtggccctgt ccttcttcat attcgagcgt 400
tgggagtgca ctacgttattg gtacatTTT gtcttctgca gtgccttcc 450
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aacccctctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
ggcaaggggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggtt 600
ttcccccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
tcttgagtct gggatttatcc gcattgtatt tagtgcTTT taataaaaata 700
tgTTTGTAG taacatTAAG acttatatac agTTTtaggg gacaattaaa 750
aaaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15

Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30

Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr	Asp	Lys	Gln	Asp	Ile	Gln	Leu	Val	Ala	Ala	Leu	Ser	Val	Thr
				50					55					60
Leu	Gly	Leu	Phe	Ala	Val	Glu	Leu	Ala	Gly	Phe	Leu	Ser	Gly	Val
				65					70					75
Ser	Met	Phe	Asn	Ser	Thr	Gln	Ser	Leu	Ile	Ser	Ile	Gly	Ala	His
				80					85					90
Cys	Ser	Ala	Ser	Val	Ala	Leu	Ser	Phe	Phe	Ile	Phe	Glu	Arg	Trp
				95					100					105
Glu	Cys	Thr	Thr	Tyr	Trp	Tyr	Ile	Phe	Val	Phe	Cys	Ser	Ala	Leu
				110					115					120
Pro	Ala	Val	Thr	Glu	Met	Ala	Leu	Phe	Val	Thr	Val	Phe	Gly	Leu
				125					130					135
Lys	Lys	Lys	Pro	Phe										
				140										

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
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cctgggctct cccccagcctc ctgcactcg gagcggctca ggagacagaa 100
gaccggcct gctgcagccc catagtgc(cc cggaacgagt ggaaggccct 150
ggcatcagag tgcgc(ccc agc acctgagcct gccctta(cgc tatgtggtgg 200
tatgcacac ggcgggcagc agctgcaaca ccccccgcctc gtgccagcag 250
caggcccgg aatgtgcagca ctaccacatg aagacactgg gctggtgcga 300
cgtggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gcccactcag gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggtctact ggcctgcgggt gtggctcagg 500
gagccctgag gtccaaactat gtgctcaaag gacaccggga tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aaccccaactg tctccttctc caataaaagat gtagctc 697

<210> 216
<211> 196
<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
1					5				10					15
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
					20				25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
					35				40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
					50				55					60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
					65				70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
					80				85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
					95				100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
					110				115					120
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
					125				130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
					140				145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
					155				160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
					170				175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
					185				190					195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggc catctgtggc caggatgtat gtcctcccg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cgccccccgg tgcctcggaa 200

gcggggccac atctcaccta agtcccggcc catggccaat tccactctcc 250
tagggctgct ggccccgcct ggggaggcgtt ggggcattct tgggcagccc 300
cccaaccgccc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac agggaaagatt gtggaccatg gcaatggac cttcagcgtc 450
cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
gccccccagt aaagctgttag agttccacca ggaacagcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggaccc tcgttgcacc cacgaccagg ccaagatctg 650
ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700
tcaaagtctgt ctgtgtctac atcgcccttct acagcacgga ctatcggtcg 750
gtccagaagg tgtgcccaga ttacaactac catagtgata cccccctacta 800
cccatctggg tgacccgggg cagggccacag agggccaggcc agggctggaa 850
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaagg 900
gttgggcctc aggcaaggag ggggggtggag acgaggagat gccaagtggg 950
gccagggcca agtctcaagt ggcagagaaa gggtcccaag tgctggccc 1000
aacotgaagc tgtggagtga ctagatcaca ggagcaactgg aggaggagtg 1050
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ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
gtcatggag gaagctaagc cttgggttct tgccatcctg aggaaagata 1200
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
atggatggct gagagggcgtt cctaggagcc agtcagcagg gtgggggtggg 1300
gccagaggag ctctccagcc ctgcctagtg ggcccccgtga gccccttgc 1350
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gtcttgcacag attgaccatc tgtctccagc caggccaccc ctccaaaaa 1450
ttccctcttc tgccagttact cccctgtac cacccattgc tcatggcaca 1500
cccatcctta agctaagaca ggacgattgt ggtcccccacca cactaaggcc 1550
acagcccatc cgccgtgtgt gtgtccctct tccaccccaa cccctgctgg 1600
ctccctctggg agcatccatg tccggagag gggtccctca acagtcagcc 1650

tcacctgtca gaccggggtt ctccggatc tggatggcgc cgccctctca 1700
gcagcggca cgggtggggc ggggccggc cgcagagcat gtgctggatc 1750
tgttctgtgt gtctgtctgt ggggtggggg aggggaggga agtcttgta 1800
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
aataaagctt gccccgggc a 1871

<210> 218
<211> 252
<212> PRT
<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
1					5				10			15		
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
					20				25			30		
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
					35				40			45		
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met
					50				55			60		
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala
					65				70			75		
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro
					80				85			90		
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe
					95				100			105		
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly
					110				115			120		
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln
					125				130			135		
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro
					140				145			150		
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile
					155				160			165		
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu
					170				175			180		
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro
					185				190			195		
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp
					200				205			210		

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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gcaggggccc caggcaggcc tgattcttgg gcggaggaga gtagggtaaa 100
gggttctgca tgagtcctt aaaggacaaa ggtaacagag ccagcgagag 150
agctcgaggg gagactttga cttcaagcca cagaatttgtt ggaagtgtgc 200
gcgcgcgcgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250
tcttcccgag caccgggatc ccggggtagg aggacgcgcg ggcgagcacc 300
agcgccagcc ggctgcggct gcccacacgg ctcaccatgg gctccggcg 350
ccgggcgtg tccgcgggtgc cggccgtgct gctggtcctc acgctgccgg 400
ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
aagtgtctgg tgggtgtgaca ctcgaacccg gccacggact ccaagggttc 500
ctcttcctcc ccgctggga tatcggtccg ggcggccaac tccaagggtcg 550
ccttctcgcc ggtgcggagc accaaccacg agccatccga gatgagoaac 600
aagacgcgca tcatttactt cgatcagatc ctggtaatg tggtaattt 650
ttcacattt gagtctgtct ttgttagcacc aagaaaagga atttacagtt 700
tcagtttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
ttgatgttaa atggaaaacc agtaatatct gccttgccg gggacaaaga 800
tgttactcgt gaagctgcca cgaatgggtgt cctgctctac ctagataaag 850
aggataaggt ttacctaaaa ctggagaaag gtaatttgtt tggaggctgg 900
cagtattcca cgtttctgg ctttctgggtt tccccctat aggattcaat 950
ttctccatga tggtcatcca ggtgagggat gaccactcc tgagttattt 1000
gaagatcatt ttttcatcat tggattgatg tcttttattt gtttctcatg 1050
ggtgatgtatg gattctaagg attcttagcct gtctgaacca atacaaaatt 1100

tcacagatta tttgtgtgtc tctgtttcag tatatttggaa ttgggactct 1150
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acttattctg aatttcattt cctgggattt ctgaattagt tacagatgtg 1250
gaattttatt tgtagtttt taaaagactg gcaaccaggta ctaaggatta 1300
gaaaactcta aagttctgac ttcaatcaac ggtagtgtg atactgccaa 1350
agaactgtat actgtgttaa tatattgatt atatttgtt ttattccctt 1400
ggaatttagtt tgtagttttc ttgtaaaaaaaaa cttggatttt tttttcagt 1450
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aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaaa 1550
aatgtctca tagttgtatt ttaattgtat atgtgaaaga gtcataatttt 1600
ccaagttata ttttctaaga agaagaatag atcataaatac tgacaaggaa 1650
aaagttgctt accaaaaatc taagtgtca atccctgagc ctcagcaaaa 1700
cagctccccct ccgagggaaa tcttatactt tattgctcaa ctttaattaa 1750
aatgattgat aataaccact ttataaaaaaaaa cctaaggaaa ttttttttc 1800
cgttagacatg accactttat taactggtgg tggatgctg ttgtttctaa 1850
ttataccat ttttcaaggc ttctgttgta tttgaagttt catctggttt 1900
tgccttaact ctttaatttgc tatataattttt tctgttttagc taatattaaa 1950
ttcaaatatc ccatatctaa atttagtgca atatcttgc ttttttatag 2000
gtcatatgaa ttcataaaat tattttagtc tgtagatagaa taaagattaa 2050
tatatgttaa aaaaaa 2065

<210> 220
<211> 201
<212> PRT
<213> Homo sapiens

<400> 220
Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
1 5 10 15
Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
20 25 30
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
35 40 45
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
50 55 60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala
				65					70					75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr
				80					85					90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe
				95					100					105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr
				110					115					120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile
				125					130					135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe
				140					145					150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val
				155					160					165
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu
				170					175					180
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly
				185					190					195
Phe	Leu	Val	Phe	Pro	Leu									
				200										

<210> 221

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 221

acggctcacc atgggctccg 20

<210> 222

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 222

aggaagagga gcccttggag tccg 24

<210> 223

<211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tgggtgggtgc cgactcgAAC 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly	
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				20				25							30
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35				40							45
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	
				50				55							60
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	
				65				70							75
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	
				80				85							90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	
				95				100							105
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	
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Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	
				125				130							135
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	
				140				145							150
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	
				155				160							165
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	
				170				175							180
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	
				185				190							195
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	
				200				205							210
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	
				215				220							225
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	
				230				235							240
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	
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Ser	Arg														

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
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agttttagcg cacctacgtg gacgaggta acagcgagct ggtcaacatc 200
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
									25					30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser
							35			40				45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn
					50				55					60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln
					65				70					75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val
					80				85					90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg
					95				100					105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro
					110				115					120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser
					125				130					135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg
					140				145					150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn
					155				160					165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu
					170				175					180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe
					185				190					195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr
					200				205					210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met
					215				220					225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser
					230				235					240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala
					245				250					255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro
					260				265					270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser
					275				280					285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys
					290				295					300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala
					305				310					315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala

320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala 335	340	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly 350	355	360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser 365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe 380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val 395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys 410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala 425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe 440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val 455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn 470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly 485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile 500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile 515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu 530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr 545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys 560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met 575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro 590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile 605	610	615

Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn
 620 625 630
 Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
 635 640 645
 Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu
 650 655 660
 Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
 665 670 675
 Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
 680 685 690
 Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr
 695 700 705
 Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala
 710 715 720
 Ile Gly Ile Cys Asn Leu Leu Tyr Phe Ala Phe Tyr Ile Ile
 725 730 735
 Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu
 740 745 750
 Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe
 755 760 765
 Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser
 770 775 780
 Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
 785 790 795
 His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser
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 Arg Asp Lys Ile Tyr Val Phe
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<210> 228
 <211> 2848
 <212> DNA
 <213> Homo sapiens

<400> 228
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Glu Asn Tyr Gly Gly Asn Phe Pro Leu Tyr	Leu Thr Lys Leu Pro	
35	40	45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile	Val Leu Ser Gly Asp	
50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala	Met Asp Pro Asp Ser	
65	70	75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp	Arg Glu Glu Gln Ala	
80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met	Gln Asp Gly His Val	
95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val His	Val Lys Asp Glu Asn	
110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala Ile	Tyr Arg Ala Arg Leu	
125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe	Leu Phe Leu Glu Ala	
140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn	Ser Asp Leu Arg Phe	
155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro	Ser Pro Asp Met Phe	
170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala	Leu Ser Pro Lys Gly	
185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg	Thr Tyr Gln Leu Leu	
200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala	Ser Gly His Gln Ala	
215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile	Glu Ser Thr Trp Val Ser	
230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu	Lys Val Leu Tyr Pro	
245	250	255
His His Met Ala Gln Val His Trp Ser Gly	Gly Asp Val His Tyr	
260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe	Glu Val Asn Ala Glu	
275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp	Arg Glu Ala Gln Ala	
290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn	Ser His Gly Glu Asp	
305	310	315

Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn
 320 325 330
 Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile
 335 340 345
 Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
 350 355 360
 Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr
 365 370 375
 Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala
 380 385 390
 Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu
 395 400 405
 Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met
 410 415 420
 Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val
 425 430 435
 Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile
 440 445 450
 Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro
 455 460 465
 Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu
 470 475 480
 Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr
 485 490 495
 Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val
 500 505 510
 Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser
 515 520 525
 His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly
 530 535 540
 Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val
 545 550 555
 Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu
 560 565 570
 Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr
 575 580 585
 Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu
 590 595 600
 Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp		
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu		
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His		
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
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Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val		
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<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgccttaccg cgcaagccga agattcacta tggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Segeunce

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
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cagaaatgga gacgagatca gcaaattttag tcaactatgt aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200
gatgtcctgg tccccatctgt cagtcgtcag gcatttaat ctttcctgag 250
atcccagggc tttagtgacg cagtgacaat tgaggacctg caggcccttt 300
tagacaatga agatgtatgaa atgcaacaca atgaagggcga agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaaat ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
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ccaataaaata ttcaatgtga aaaaaaaaaa aaaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens .

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
1				5					10					15
Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
					20				25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
					35				40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
					50				55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
					65				70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
					80				85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
					95				100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
					110				115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
					125				130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
					140				145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
					155				160					165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile
				170					175				180	
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala
				185					190				195	
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser
				200				205				210		
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro
				215				220				225		
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys
				230				235				240		
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro
				245				250				255		
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp
				260				265				270		
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu
				275				280				285		
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn
				290				295				300		
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met
				305				310				315		
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu
				320				325				330		
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val
				335				340				345		
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr
				350				355				360		
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile
				365				370				375		
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly
				380				385				390		
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr
				395				400				405		
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu
				410				415				420		

Tyr

<210> 235
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 235

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cccgcccttc ctccacaaag agcacccctg cctcacaggt gtattccctc 200
aacaccgact ttgccttccg cctataccgc aggctggtt tggagacccc 250
gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300
tgctctccct tggggcccac tcagtcacca agacccagat tctccaggc 350
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gccctttcac cttgaatata caagaaagaa cttcccatcc ctggtggcgc 750
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ctccagaaaaa ggtggataga ggtgttcatc cccagatttt ccatttctgc 1000
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aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
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Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
				20				25					30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
				35				40					45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
				50				55					60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
				65				70					75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
				80				85					90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
				95				100					105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
				110				115					120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
				125				130					135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
				140				145					150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
				155				160					165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
				170				175					180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
				185				190					195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala

	200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe			
215	220	225	
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met			
230	235	240	
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn			
245	250	255	
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe			
260	265	270	
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala			
275	280	285	
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys			
290	295	300	
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser			
305	310	315	
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala			
320	325	330	
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser			
335	340	345	
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser			
350	355	360	
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile			
365	370	375	
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn			
380	385	390	
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile			
395	400	405	
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser			
410	415		

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

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<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
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<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgaaa tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggatataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tggtggcctc tgtgtcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
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ctttctcaag aatcctctgt tcttgcctt ctaaagtctt ggtacatcta 200
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cgtggggctc tttgctggc tcttctctg tgtgagaaac agcctgtccc 1850
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aatactatat tgctcatatta gctaagaaat aaatacatct catctaacac 2250
acacgacaaa gagaagctgt gcttgcccg gggtggtat ctagctctga 2300
gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaaaaaa 2400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5				10					15	
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70					75	

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
 80 85 90

 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 110 115 120

 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
 125 130 135

 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
 140 145 150

 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 155 160 165

 Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
 170 175 180

 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 185 190 195

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 200 205 210

 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 215 220 225

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 230 235 240

 Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
 245 250 255

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 260 265 270

 Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 275 280 285

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 290 295 300

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 305 310 315

 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
 320 325 330

 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 335 340 345

 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
 350 355 360

 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala 380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala 395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala 410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala 425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val 440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala 455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala 470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala 485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile 500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe 515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn 530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly 545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro 560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile 575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro 590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26
<210> 245
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic sequence.

<400> 245
gtcagagttg gtggctgtgc tagc 24
<210> 246
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 246
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48
<210> 247
<211> 957
<212> DNA
<213> Homo sapiens

<400> 247
gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50
ttcccgacct tcccagcaat atgcatcttg cacgtcttgt cggtccctgc 100
tccctccttc tgctactggg ggcctgtct ggatggcg 150
ccccatttag aaggtcattt aaggatcaa ccgagggtcg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcatt 250
gcggaaagg aagtggagaa ggtttcaac ggacttagca acatggggag 300
ccacacccggc aaggagttgg acaaaggcgt ccagggctc aaccacggca 350
tggacaagg tggccatgag atcaaccatg gtattggaca agcaggaaag 400
gaagcagaga agcttggcca tgggtcaac aacgctgctg gacaggccgg 450
gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500
ctggaaagg agcagagaaa cttggccaag gggtaacca tgctgctgac 550
caggctggaa aggaagtgg aagcttggc caaggtggcc accatgctgc 600

tggccaggcc gggaggagc tgcagaatgc tcataatggg gtcaacccaag 650
ccagcaagga ggccaaccag ctgctaatg gcaaccatca aagcgatct 700
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
agtcaacacg ccttcatca accttcccgc cctgtggagg agcgtcgcca 800
acatcatgcc ctaaactggc atccggcctt gctggagaa taatgtcgcc 850
gttgcacat cagctgacat gacctggagg gttgggggt gggggacagg 900
tttctgaaat ccctgaaggg gttgtactg ggatttgtga ataaacttga 950
tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	
1					5				10				15	
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu
				20					25				30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg
				35					40				45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His
				50					55				60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met
				65					70				75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu
				80					85				90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile
				95					100				105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn
				110					115				120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln
				125					130				135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys
				140					145				150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu
				155					160				165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala
				170					175				180	

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Pro Leu Ala Ser Gly
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240

Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttccttcc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgaccattt gagaaggta ttgaaggat caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252
ctccgggtcc ccaggggctg cgccgggccc gcctggcaag ggggacgagt 50
cagtggacac tccaggaaga gcggccccgc gggggggcgat gaccgtgcgc 100
tgacctgac tcactccagg tccggaggcg gggggccccc gggcgactcg 150
ggggcggacc gcggggcgga gctgccccc gtgagtccgg ccgagccacc 200
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ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccc 300
cctcggccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350
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gtctgaagaa ttactgttta aaaaaaaaaa a 3781

<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
1 5 10 15

Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu
20 25 30

Leu Leu Leu Leu Leu Gln Pro Pro Pro Thr Trp Ala Leu Ser
35 40 45

Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
50 55 60

Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
65 70 75

Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80	85	90
Phe Ala Leu Ser Ser Asn Leu Ser Phe		
95	100	105
Gly Glu Gly		
Gln Glu Leu Leu Trp	Gly Ala Asp Ala	Glu Lys Lys Gln Gln Cys
110	115	120
Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp	Cys Gln Asn Tyr Ile	
125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser His	Leu Phe Thr Cys Gly	
140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu Asn	
155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val	Leu Leu Glu Asp	
170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn	Phe Lys Ser Thr Ala	
185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser Phe	
200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser	Gln Ser Leu Arg Pro	
215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala Phe	
230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu	Gly Ser Leu Gln Gly	
245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Ser	Glu Thr Gly Gln Glu	
260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg Ile	
275	280	285
Cys Lys Gly Asp Glu Gly Glu Arg Val	Leu Gln Gln Arg Trp	
290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp Asp	
305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp Val	Phe Thr Leu Ser Pro	
320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe Thr	
335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys Val	
350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr Lys	
365	370	375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro
380 385 390

Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg
395 400 405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu
410 415 420

Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser
425 430 435

Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala
440 445 450

Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe
455 460 465

Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
470 475 480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly
485 490 495

Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
500 505 510

Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
515 520 525

Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
530 535 540

Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
545 550 555

Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
560 565 570

Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser
575 580 585

Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
590 595 600

Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser
605 610 615

Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn
620 625 630

Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
635 640 645

Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
650 655 660

Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro		
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys		
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val		
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe		
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln		
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu		
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr		
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro		
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile		
800	805	810
Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg		
815	820	825
Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val		
830	835	

<210> 254
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 254
agccccgtgca gaatcttgctc ctgg 24

<210> 255
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 255
tgaagccagg gcagcgtcct ctgg 24

<210> 256
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 256
gtacaggctg cagttggc 18

<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 257
agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 258
gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
ctaagccgga ggatgtgcag ctggggcgcc ggcggccggct acgaagagga 50
cggggacagg cggccgtgcga accgagccca gccagccgga ggacgcgggc 100
agggcgggac gggagccgg actcgtctgc cgccgcccgtc gtcgcccgtcg 150

tgccggcccc gcgtccccgc gcgcgagcgg gaggagccgc cgccacctcg 200
cgccc gagcc gccgctagcg cgccggggc atggtccct cttaaaggcg 250
caggccgcgg cggcggggc gggtgtgcgg aacaaagcgc cggcgcgggg 300
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ggcggcggcg gcggccggc gggcggagcg gcgcggcat ggccgcgcgc 500
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gaaacataca cacatacacc ctaatcaaaa cggtggggaa aaatgttattt 3950
ggttttgttc ct当地区的水文特征，如流速、流量、含沙量等，以及该地区的植被、土壤和气候条件。这些信息对于理解河流的自然状态和人类活动对河流的影响至关重要。

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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val
 245 250 255
 Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
 260 265 270
 Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys
 275 280 285
 Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
 290 295 300
 Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu
 305 310 315
 His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
 320 325 330
 Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser
 335 340 345
 Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro
 350 355 360
 Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu
 365 370 375
 Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly
 380 385 390
 Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu
 395 400 405
 Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala
 410 415 420
 Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly
 425 430 435
 Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp
 440 445 450
 Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val
 455 460 465
 Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
 470 475 480
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys
 485 490 495
 Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser
 500 505 510
 Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu
 515 520 525
 His Lys Glu Pro Lys Asp Lys Ile Asn Ile Leu Ile Pro Leu

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu		
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu		
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp Lys Ala Lys Gln Val Glu		
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr Pro Lys Ala Asp Met Gln		
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser Arg Ala Leu Ala Leu Glu		
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu Ser Leu Leu Phe Phe Cys		
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu Phe Leu Gln Arg Cys Arg		
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe Pro Ile Ile Phe		
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys Val Pro Ser		
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp Arg Asn		
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val Arg		
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp		
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe		
725	730	735
Arg Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe		
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly		
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met		
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn		
785	790	795
Asn Gly Ser Val Arg Thr Ala		
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<210> 261
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
tgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtgggc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
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<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tccttctagt tgcgcttttgc tcatggcctt cgtctgtgcc ggcttatccg 200
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agtttttagag aaccttagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaaatc taactctcca aaacatgtttt attctatagc atcaaaggga 350
tcaaaaatcta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaacttgc cctacaggag 450
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tggtcgatca aaccaaacaa tgttccatt gtttgcatt cagaggaacc 550
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20				25					30	

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35				40					45	

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys	Gly Ser Lys Phe Lys	
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr	Glu Asn Asp Val Leu	
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr	Phe Pro Thr Gly Gly	
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys His	Thr Glu Ser Thr Pro	
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val	Ser Ile Val Leu His Ala	
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu	Pro Glu Pro Glu Pro Glu	
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg	Met Leu Pro Val Val	
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val	Thr Ser Tyr Lys Ser Pro	
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly	Ile Glu Ile Ser Thr Glu	
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly	Glu Thr Ala Ile Glu Lys	
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser	Trp Asn Asn Asp Asp	
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn	Ser Gln Val Gln Gln Ala	
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala	Tyr Arg Glu Asp Ile Glu	
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser	Leu Ala Leu Ala Ala Ala	
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr	Lys Ser Gln Leu Leu Pro	
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp	Asp Ile Glu Thr Val Ile	
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys	Leu Tyr Glu Tyr Leu Asp	
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg	Glu Lys Ala Ala Thr Val	
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg	Ser Arg Arg Val Thr Ala	
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Leu Leu Lys Val Tyr
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<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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aaa 2403

<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

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35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe		
50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser		
65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp		
80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr		
95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile		
110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly		
125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile		
140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala		
155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg		
170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile		
185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu		
200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu		
215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu		
230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile		
245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp		
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys		
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
305	310	315

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
		320				325						330		
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val
		335				340						345		
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp
		350				355						360		
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn
		365				370						375		
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr
		380				385						390		
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr
		395					400					405		
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe
		410				415						420		
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
		425				430						435		
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr
		440				445						450		
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp
		455				460						465		

Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
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tcatttatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
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agttcagtca acagaagcat ggagtgttgg ctcatatgtc gttgatttgt 400
agatttcact ctactgagga tcctgaaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcaactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggAAC acgaagaagt aaaactctag gtcagagtct 600
caggatcgTT ggtgggacag aagtagaaga gggtaatgg ccctggcagg 650
ctagcctgca gtggatggg agtcatcgct gtggagcaac cttaattaat 700
gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750
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catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
aaatgcagta catagagttt gtctccctga tgcacccatg gagtttcaac 950
caggtgatgt gatgtttgtg acaggattt gggactgaa aaatgtatgg 1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
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tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

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caaacttcat gcaatgtact tgttctaaggc aaattaaagc aaatatttat 2050
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cca 2103

<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269
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35 40 45
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210
Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
215 220 225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230			235					240		
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245			250				255			
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260			265			270				
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275			280			285				
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290			295			300				
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305			310			315				
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320			325			330				
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335			340			345				
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350			355			360				
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365			370			375				
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380			385			390				
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395			400			405				
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410			415			420				

Thr Gly Ile

<210> 270
<211> 1170
<212> DNA
<213> Homo sapiens

<400> 270
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cagacgtcag ctggtgatt cccgctgcat caaggcctac ccactgtctc 150
catgctggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
ttccccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgccttg ccggctgtcc cctgcgacta 300
cgaccactgc cgacacotgc aggtgccctg caaggagcta cagagggtcg 350
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
gaccggccgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450
agtggtccac tggtgtgccc ctttcctccc ggtcctccac tactggctgc 500
tgctttggaa cggcagcggag gctgcgcaga agggggccccc gctgaacgct 550
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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
					20				25					30

Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35					40					45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
				50				55						60

Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
				65				70						75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
 80 85 90
 Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
 95 100 105
 Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
 110 115 120
 Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
 125 130 135
 Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
 140 145 150
 Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
 155 160 165
 Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
 170 175 180
 Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
 185 190 195
 Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
 200 205 210
 Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
 215 220 225
 Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
 230 235

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
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 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
					20				25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35				40						45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50				55						60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65				70						75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80				85						90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95				100						105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110				115						120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125				130						135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140				145						150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155				160						165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln		
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
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Glu Met Glu Glu Leu		
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<211> 2063		
<212> DNA		
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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp
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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
	20				25						30			

Lys	Val	Gly	Ile	Pro	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser	
	35						40					45		

Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
	50						55					60		

Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
	65				70				75					

Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
	80				85				90					

His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
	95				100				105					

Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
	110				115				120					

Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
	125				130				135					

Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
	140				145				150					

Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
	155				160				165					

Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
	170				175				180					

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
	185				190				195					

Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
	200				205				210					

Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
	215				220				225					

Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
	230				235				240					

Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
	245				250				255					

Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys
260 265 270

Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
275 280 285

Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr
290 295 300

Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
305 310 315

Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn
320 325 330

Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
335 340 345

Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu
350 355 360

Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val
365 370 375

Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
380 385 390

Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys
395 400 405

Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
410 415 420

Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu
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<210> 276
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 276
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gagcatggcc ctcccagccc tgggcctgga cccctggagc ctcctgggcc 150
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aagcatacgg ctgtcttgggt ggatgggatg ctctattctg gtactatgaa 700
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<210> 277
<211> 761
<212> PRT
<213> Homo sapiens

<400> 277

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Ala Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60

Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
 200 205 210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
 215 220 225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 230 235 240

Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
 245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
 260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
 275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro		
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val		
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp		
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu		
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg		
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr		
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr		
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val		
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr		
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly		
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp		
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala		
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala		
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg		
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu		
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg		
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser		
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala		
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala		
575	580	585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

ctgctggta aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgtcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
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tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
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<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282
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Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
 20 25 30

Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
 35 40 45

Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
 50 55 60

Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
 65 70 75

Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
 80 85 90

Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
 95 100 105

Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
 110 115 120

Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
 125 130 135

Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
 140 145 150

Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
 155 160 165

Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
 170 175 180

Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
 185 190 195

Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
 200 205 210

Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
 215 220 225

Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
 230 235 240

Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
 245 250 255

Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn		
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu		
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu		
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys		
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn		
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His		
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile		
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu		
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys		
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu		
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser		
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser		
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr		
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp		
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu		
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala		
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr		
515	520	

<210> 283

<211> 24

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
 tgccttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
 tcaggctggc ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
 cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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ccacccctcctg aaactgctcc acctttgaag tttgaacttt agtcccctcca 1950
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agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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Pro	Gly	Leu	Pro	Leu	Val	Ileu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
		20						25				30		
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Ileu	Glu	Gly	Glu	Cys
		35						40				45		
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
		50						55				60		
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
		65						70				75		
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
		80						85				90		
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Ileu	Val	Asn	Glu
		95							100				105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
		110							115				120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
		125							130				135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Ileu	Met	Ileu	Asn	Thr	Trp	Pro	Val
		140						145				150		
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
		155							160				165	
Thr	Ser	Ser	Val	Ileu	Ileu	Pro	Ileu	Asp	Pro	Gly	Asp	Arg	Val	Ser

170 175 180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
200 205

<210> 288

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-27

<223> Synthetic construct.

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-42

<223> Synthetic construct.

<400> 290

ctgtgtact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50

tagccgcccc gcctcgacgc cgtcccgaaa cccctgtgt ctgcgcgaag 100

ccctggcccc gggggccggg gcatggcca gggggcgcggg gtgaagcggc 150

ttcccgccgg ggcgtgactg ggccggcttc agccatgaag accctcatag 200
ccgcctactc cggggtcctg cgccgcgagc gtcaggccga ggctgaccgg 250
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<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292
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Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
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Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45

Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60

Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75

Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90

Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105

Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120

Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135

Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150

Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165

Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
 185 190 195

Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
 200 205 210

Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
 215 220 225

Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Val Val Gly Gly
 230 235 240

Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
 245 250 255

Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 295

aagaatgaat tgtacaaagc aggtgatctt cgaggaggcc tcctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggcggcggg atggggcccg ggggcggcgg gcgcgcact cgctgaggcc 50

ccgacgcagg gccgggcccgg gcccaggggcc gaggagcgcg gcggccagag 100

cggggccgcg gaggcgcacgc cggggacgc cgcgcgcacga gcaggtggcg 150

gcggctgcag gcttgcgtccag ccggaagccc tgagggcagc tgttccact 200

ggctctgctg accttgcgtcc ttggacggct gtcctcagcg agggccgtg 250

caccgcgtcc tgagcagcgc catgggcctg ctggccctcc tgaagaccca 300

gttgcgtgcgt cacctgcgtgg tcggctttgt cttcgtggcg agtggctgg 350

tcatcaactt cgtccagctg tgcacgcgtgg cgctctggcc ggtcagcaag 400

cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450

actggtcatg ctgctggagt ggtggcctg cacggagtgt acactgttca 500

cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550

ctcaaccaca acttcgagat cgacttcctc tgggggtggaa ccatgtgtga 600

gchgcttcgga gtgctggga gctccaaggt cctcgctaag aaggagctgc 650

tctacgtgcc cctcatcggt tggacgtggt acittctggaa gattgtgttc 700

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tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggccatg 1150

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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu
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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe
					20				25				30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu
					35				40				45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln
					50				55				60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu
					65				70				75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala
					80				85				90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly
					95				100				105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val
					110				115				120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr
					125				130				135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu
					140				145				150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr
					155				160				165	

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
 170 175 180
 Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
 185 190 195
 Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
 200 205 210
 Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
 215 220 225
 Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
 230 235 240
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
 245 250 255
 Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
 260 265 270
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
 275 280 285
 Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
 290 295 300
 Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
 305 310 315
 Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
 320 325 330
 Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
 335 340 345
 Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
 350 355 360
 Glu Pro Gly Arg Trp Arg Leu Gln
 365

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299
gccacacctcca tgctaaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300
ccaaggtcct cgctaaagaag gagctgctct acgtgccctt catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301
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tcagtttgc ttgtggggtt ggtggcaggc aggccggctt acgcctgata 200
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acagagtgag actctatgtc caaaaaaaaaaaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
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His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20						25				30	
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40				45	
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55				60	
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70				75	
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85				90	
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100				105	
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115				120	
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130				135	
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

<400> 303
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<211> 109
<212> PRT
<213> Homo sapiens

<400> 304
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Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
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Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
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Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
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Arg Arg Arg Asp

<210> 305
<211> 989
<212> DNA
<213> Homo sapiens

<400> 305

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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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					20				25				30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
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Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50				55					60	

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu
				65					70					75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln
				80					85					90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys
				95					100					105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu
				110					115					120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val
				125					130					135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala
				140					145					150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu
				155					160					165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp
				170					175					180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr
				185					190					195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val
				200					205					210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly
				215					220					225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg
				230					235					240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly
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<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

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Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe
35 40 45

Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60

Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75

Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90

Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105

Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120

Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135

Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Lys Ser Ser

140	145	150
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155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala		
170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu		
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala		
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys		
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser		
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser		
245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val		
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro		
275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser		
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu		
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg		
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Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln		
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg Glu Arg Ala Asp Arg Gly		
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Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg		
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly		
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu		
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser		
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg		
425	430	435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
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 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
 455 460 465
 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
 470 475 480
 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
 485 490 495
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
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 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
 515 520 525
 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
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 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
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 Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
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 Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
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 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
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 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
 620 625 630
 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
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<210> 309

<211> 3871

<212> DNA

<213> Homo sapiens

<400> 309

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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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				20				25				30		

Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
				35				40				45		

Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	
				50				55				60		

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
				65				70			75			

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80	85	90
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Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn		
125 130		135
Gln Pro Tyr Asn Lys Thr His Ile Tyr Val		
140 145		150
Phe His Pro Ile Cys Gly Tyr Ile Asp Leu		
155 160		165
Asp Ile Ile Phe Lys Leu Asp Thr His Asn		
170 175		180
Leu Lys Cys Pro Phe Asp Pro Gln Gln Pro		
185 190		195
Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala		
200 205		210
Lys Asp Thr Ala Phe Thr Arg Ser Leu Gly		
215 220		225
His Tyr Ile Arg Thr Asp Ile Ser Glu His		
230 235		240
Ala Lys Phe Ile Gly Thr Phe Phe Ile Pro		
245 250		255
Asp Asp Asp Lys Ile Tyr Phe Phe Arg Glu		
260 265		270
Gly Ser Thr Ser Asp Lys Thr Ile Leu Ser		
275 280		285
Cys Lys Asn Asp Val Gly Gly Gln Arg Ser		
290 295		300
Thr Thr Phe Leu Lys Ala Arg Leu Ile Cys		
305 310		315
Asp Gly Ala Asp Thr Tyr Phe Asp Glu Leu		
320 325		330
Leu Pro Thr Arg Asp Glu Arg Asn Pro Val		
335 340		345
Thr Thr Thr Ser Ser Ile Phe Lys Gly Ser		
350 355		360
Ser Met Ala Asp Ile Arg Ala Val Phe Asn		
365 370		375

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
 380 385 390
 Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro
 395 400 405
 Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe
 410 415 420
 Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
 425 430 435
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
 440 445 450
 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
 455 460 465
 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
 470 475 480
 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
 485 490 495
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 515 520 525
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 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
 545 550 555
 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
 560 565 570
 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
 575 580 585
 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
 590 595 600
 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
 605 610 615
 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
 620 625 630
 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
 635 640 645
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
 650 655 660
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

665	670	675
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Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu		
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu		
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp		
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp		
740	745	750
Lys His Met Gln Glu Met Lys Lys Arg Asn Arg Arg His His		
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr		
770	775	

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<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 311
caacgcagcc gtgataaaca agtgg 25

<210> 312
<211> 24
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<220>
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<222> 1-24
<223> Synthetic construct.

<400> 312
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<210> 313
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<222> 1-45
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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														15

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Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala
 35 40 45

Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
 50 55 60

Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
 65 70 75

Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
 80 85 90

Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
 95 100 105

Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
 110 115 120

Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
 125 130 135

Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
 140 145 150

Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
 155 160 165

Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
 170 175 180

Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
 185 190 195

Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
 200 205 210

Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
 215 220 225

Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
 230 235 240

Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
 245 250 255

Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
 260 265 270

Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
 275 280 285

Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
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Gln Met Leu Pro Ser Pro Ser Pro Ser Phe Ser Pro Pro Ala

305 310 315

Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly
320 325 330

Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro
335 340 345

Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Ala Lys Ala
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Pro Asp Pro Gly His Pro Asp Pro Leu Thr
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
20 25 30

Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45

Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60

Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75

Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90

Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105

Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120

Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135

Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

140	145	150
Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro	Leu
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His	Ile
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys	Asn
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg	Ala
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val	Val
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys	Arg
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Ala Lys Ala Phe Lys	His
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu	Val
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser	Ala
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu	Asn
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile	Leu
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr	Leu
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser	Cys
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala	Ala
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser	Lys
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His	Val
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp	Ser
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly	Tyr
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu	Pro
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
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 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
 455 460 465
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
 485 490 495
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
 500 505 510
 Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
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 Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Val
 530 535 540
 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
 545 550 555
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
 560 565 570
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
 575 580 585
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
 590 595 600
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
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 620 625 630
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
 635 640 645
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 650 655 660
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
 665 670 675
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
 680 685 690
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
 695 700 705
 Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
 710 715 720
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

725 730 735

Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp
740 745 750

Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr
755 760 765

Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro
770 775 780

Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg
785 790 795

Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro
800 805 810

Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu
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Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys
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<210> 318

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 318

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<210> 319

<211> 24

<212> DNA

<213> Artificial

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<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 319

ctgtgctttt cggtgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 320
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<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

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<210> 322

<211> 317
<212> PRT
<213> Homo sapiens

<400> 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
		20						25							30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
			35					40							45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50				55							60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65				70							75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80				85							90
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95				100							105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110				115							120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125				130							135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140				145							150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155				160							165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170				175							180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185				190							195
Leu	Gln	Asp	Phe	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala		
				200				205							210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215				220							225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230				235							240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245				250							255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260				265							270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300
Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315
Arg Val

<210> 323
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 323
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ggccgtgcag cttctggct tcctgctcag cttcctggc atggtggca 150
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accaacatcc tcacggccgt gtcctacctg aaagggtctt ggatggagt 250
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tgcctgctct cgggcatacg ctgcgcctgc gccgtcatcg ggatgaagt 400
cacgcgtgc gccaaggca caccgccaa gaccacctt gccatcctcg 450
gcggcaccct cttcatcctg gccggcctcc tgtgcattgtt ggccgtctcc 500
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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
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Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp
					20				25				30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser
					35				40				45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly
					50				55				60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln
					65				70				75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu
					80				85				90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr
					95				100				105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu
					110				115				120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala
					125				130				135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro
					140				145				150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr
					155				160				165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu
					170				175				180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln
					185				190				195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	
					200				205				210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val
					215				220				225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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cacatgccaa gtggtggcgt tcctctgtc catcctgggg ctggccggct 150
gcatcgccgc caccggatg gacatgtgga gcacccagga cctgtacgac 200
aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

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Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
20 25 30

Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
35 40 45

Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
50 55 60

Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
65 70 75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg		
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr		
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly		
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser		
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly Met Val Gln Thr Val		
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val		
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala		
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser		
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe		
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile		
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro		
245	250	255
Ser Lys His Asp Tyr Val		
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<210> 327

<211> 2010

<212> DNA

<213> Homo sapiens

<400> 327

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cattgaaaac aacatcgtgg ttttgaaaa cttctggaa ggactgtgga 250
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ctgctgacgg ctggaatcat ctcatcatc acgggcatgg tggtgctcat 500
ccctgtgagc tgggttgcca atgcccatac cagagattc tataactcaa 550
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ttttctaatt 2010

<210> 328
<211> 225
<212> PRT
<213> Homo sapiens

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Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
35 40 45
Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
50 55 60
Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
65 70 75
Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
80 85 90
Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
95 100 105
Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
110 115 120
Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
125 130 135
Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
140 145 150
Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
155 160 165
Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
170 175 180
Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
185 190 195
Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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tgtttgtta gtgca 1315

<210> 330
<211> 220
<212> PRT
<213> Homo sapiens

<400> 330
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20 25 30
Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45
Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60
Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75
Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90
Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105
Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120
Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135
Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150
Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165
Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Gly Gly Gly Leu
170 175 180
Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
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200 205 210
Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331
<211> 1160
<212> DNA

<213> Homo sapiens

<400> 331

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gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtgg 200
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gcaagttcta tagtccttg ttggctctcc cgcctgcctt ggaaacagcc 350
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taagtatgtg aggcaaggaga acttgcttta tgtcttagatt tacattgata 900
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acattctgac ttcaagggtgttta ttaaatgcat tgactattgt tggacccat 1000
cgctgctcca atttcatat tctaaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
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acctattctta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg			
20	25	30	
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu			
35	40	45	
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn			
50	55	60	
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe			
65	70	75	
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala			
80	85	90	
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly			
95	100	105	
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser			
110	115	120	
Ala Ala Val Leu Phe Ile Gly Gly Leu Leu Cys Gly Phe Cys			
125	130	135	
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly			
140	145	150	
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu			
155	160	165	
Ser Lys Thr Ser Thr Ser Tyr Val			
170			

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtggtgccc atcccctgcc ccatcacata cctaccagg 200
 tgtggttctg actacatcac ctatggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
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 tcatcatccc aggctctgac tgagtttctt tcagtttac tgatgttctg 400
 ggtggggac agagccagat tcagagtaat cttgactgaa tggagaaaat 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcatttt 500
ttttaaacac gtcaataaaa aaataatctc ccaga 535

<210> 334
<211> 85
<212> PRT
<213> Homo sapiens

<400> 334
Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15
Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30
Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45
Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60
Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75
Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335
<211> 742
<212> DNA
<213> Homo sapiens

<400> 335
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tggccctgac cgggctggcg ctgctcctgc tcctgtgctg gggcccaggt 150
ggcataagtg gaaataaact caagctgatg cttcaaaaaac gagaagcacc 200
tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
cccgagggtgc agcagtggtt ccagcagttt ctctacatgg gctttgatga 350
agcgaaattt gaagatgaca tcacctattt gcttaacaga gatcgaaatg 400
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550
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tttgcttat ttcagcagat ctttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct tttgatattt catggaaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336

Met	Ala	Ala	Ser	Pro	Ala	Arg	Pro	Ala	Val	Leu	Ala	Leu	Thr	Gly
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Leu	Ala	Leu	Leu	Leu	Leu	Cys	Trp	Gly	Pro	Gly	Gly	Ile	Ser	
				20				25				30		
Gly	Asn	Lys	Leu	Lys	Leu	Met	Leu	Gln	Lys	Arg	Glu	Ala	Pro	Val
				35				40				45		
Pro	Thr	Lys	Thr	Lys	Val	Ala	Val	Asp	Glu	Asn	Lys	Ala	Lys	Glu
	.			50				55				60		
Phe	Leu	Gly	Ser	Leu	Lys	Arg	Gln	Lys	Arg	Gln	Leu	Trp	Asp	Arg
				65				70				75		
Thr	Arg	Pro	Glu	Val	Gln	Gln	Trp	Tyr	Gln	Gln	Phe	Leu	Tyr	Met
				80				85				90		
Gly	Phe	Asp	Glu	Ala	Lys	Phe	Glu	Asp	Asp	Ile	Thr	Tyr	Trp	Leu
				95				100				105		
Asn	Arg	Asp	Arg	Asn	Gly	His	Glu	Tyr	Tyr	Gly	Asp	Tyr	Tyr	Gln
				110				115				120		
Arg	His	Tyr	Asp	Glu	Asp	Ser	Ala	Ile	Gly	Pro	Arg	Ser	Pro	Tyr
				125				130				135		
Gly	Phe	Arg	His	Gly	Ala	Ser	Val	Asn	Tyr	Asp	Asp	Tyr		
				140				145						

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337

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tgaagggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
ttctgggtct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcg 200
gaccactgc cccagccgtc agggacccca acgccatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggccccca ggggcagaga 300
cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcg 400
gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagttcc cggccggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550
gaccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
tgtccacgag agtcggtccc ccaaattcccc cctgcccggc ggggtccgag 650
cccgccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
cctgctgttg ctgctgctct ggtactgcca gatccagtag cggcccttct 750
ttccctgac cgccactctg ggcctggccg gcttcacccct gtcctcagt 800
ctcctggcct ttgccatgta ccgccccgtag tgcctcccg ggcgcttggc 850
agcgctgccc gccccctccgg accttgcctcc ccgcgcggcg gcgggagctg 900
ctgcctgccc aggccccctt ctccggcctg cctcttcccc ctgccttgga 950
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tgcgaccgccc ggggctcgcc gccacccccc ggggctgctg aacccctagcc 1050
cgcaactggga gtgggctcct cggggctcgcc catctgctgt cgctgcctcg 1100
gccccggca gagccgggcc gccccgggg cccgtcttag tgttctgccc 1150
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acgccaggc ggtgggaggc tggtgaaggg gagcggggag gggcagagga 1250
gttccccgga acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
aaaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
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Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25				30	
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40				45	

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp
					50					55			60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg
					65				70			75		
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr
					80				85			90		
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu
					95				100			105		
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp
					110				115			120		
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly
					125				130			135		
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly
					140				145			150		
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys
					155				160			165		
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro
					170				175			180		
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile
					185				190			195		
Gly	Ser	Leu	Leu	Leu	Pro	Leu								
					200				205			210		
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala
					215				220			225		
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala
					230				235			240		
Phe	Ala	Met	Tyr	Arg	Pro									
					245									

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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atgacaaaagg cgctactcat ctatggtc agcagcttc ttgcctaaa 200
tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

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aggacttgga tgggttgag ggtaactccc tgagtgactg gctgtgcctg 300
gctttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagctt gactatggcc tcttcagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaacctt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccctct tcgaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cggggatga acaactgggt agaatggagg ttgcactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
agggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
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ccttccatt tacaactaaa actgaccaga gccccagaa taaatggttt 750
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tgttatttgc aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
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Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
20 25 30

Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45

Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60

Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75

Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90

Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105

Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120

Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

 <400> 341
 ccctccaagg atgacaaaagg cgc 23

 <210> 342
 <211> 29
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

 <400> 342
 ggtcagcgc tttcttgccc taaatcagg 29

 <210> 343
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 343
 atctcaggcg gcattcgtgc agcc 24

 <210> 344
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 344
 gtggatgcct gcaagaagg tggg 24

 <210> 345
 <211> 45
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
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caaaggggga aagaaaacacc tgagcagaat ggaatcatta tttttttccc 150
aaggagaaaa ccggggtaaa gggagggaaag caattcaatt tgaagtccct 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtaaac ttgggtcctg tggttttctg attgttaagtg gaagcaggtc 300
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gggttgcgg acattccact ggttctggc taatgtctac cctgagctgt 1950
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
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Phe Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
260 265 270

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
275 280 285

Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
290 295 300

Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
305 310 315

Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
320 325 330

Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
335 340 345

Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
350 355 360

Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr
365 370 375

Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly
380 385 390

Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly
395 400 405

Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln
410 415 420

Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg
425 430 435

Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu
440 445 450

Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala
455 460 465

Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
470 475 480

Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu
485 490 495

Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His
500 505 510

Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp
515 520 525

Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg
530 535 540

Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val		
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln		
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser		
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu		
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe		
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

Sequence Data from Human Genome Project

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<210> 348
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 348
ggagaggtgg tggccatgga cag 23

<210> 349
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 349
ctgtcactgc aaggagccaa cacc 24

<210> 350
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 350
tatgtcgctg cgaggtggtg aaaacctcga actgtcttc aaggc 45

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<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
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tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc cccatgtgc 200
caggggaggc ccctcgcccc cacgtcatgt gtgcgtgtgg gagcagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtccctg 300
cctggcactg caccggcacc caccggatca ggctttgagg agggccgccc 350
ctcatcccaa tacccctggg ctatcggttg gggtcccacc gtgtctcgag 400
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatgg 450
tttgcagccc ctcatggct cgcaacccca caccggact cagactccat 500
gcgagggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1					5				10				15	

Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> 353
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 353
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 cggccaggat ggcatacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccggggttc tggccccgtgc ggtgctcaca gacgatgttc cacaggagcc 150
cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
ccgtggagag caccagcccc ggccgggagc ccgtggacac cggtccccca 250
gcccccacgg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgta 350
tcggcccccct gctggccacc tgcgtggtgc tggcgctcg ggtcgctcg 400
ctgagaaagt ttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
gcggcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
1				5				10					15	

Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20				25					30	

Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35				40					45	

Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50				55					60	

Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65				70					75	

Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80				85					90	

Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
					95				100				105	

Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
					110				115				120	

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

ggccgttgt tggtgcgcgg ctgaagggtg tggcgcgagc agcgtcggt 50

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gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
tctccaagaa gttctcccttc taccgccacc atgtgaacct caagtccctgg 200
tgggtggcgc acatccccgt gtcagggcgc ctgctcacccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgtat ggatcagctg 350
taccagggga agatgtactt ccccggtat ttccccaaacg agctgcgaaa 400
catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggtagctgg ggaggaggc agctctccag ggagggaccc 500
agcctagcac ctgaaggatc aatgccatca ccccgccccg acctccccta 550
atgtcccccc agaggcgctg ggagtgttgc caccgccctc ccctgaagtt 600
tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccggcc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
tggcatcttc cagtacgaga ccatctccctg caacaactgc acagactcgc 750
acgtcgccctg ctttggctat aactgcgagt agggctcagg catcacaccc 800
accctgtgcca gggccctact gtccctgggg tcccaggctc tccttggagg 850
gggctccccg ctttccacct ggctgtcatc ggtagggcgc gggccgtggg 900
ttcagggcgc caccacttcc aaggctgtgt cccacaggctc ctggcgccag 950
tggaaagtcaag ctgtccaggg ctcctgaac tacataaata actggcacaa 1000
gtaaatcccc tcctcaaacc aacacaggca gtgtgttat gtgagcacct 1050
cgtgggtgag tatgtgtgg gcacaggctg gtccttcag ctcccacgtc 1100
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<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
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His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
20 25 30

Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
35 40 45

Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
50 55 60

Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
65 70 75

Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
80 85 90

Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
95 100 105

Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
110 115 120

Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gln
125 130 135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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ttgagaaatc ctcagatggt cctggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcac atactccata 250
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cctggtagac aatgaacaac tgaattttaga ggacgaagac attgaaagca 400
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gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
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aaatcgtgaa tcagaaggaa agactccaaa ggtggaaactc tgacttctcc 850
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cttcttatcg tgcattcata ctctgtaaac ccattctgaa cacacctaga 1150
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cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
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cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
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caacctgcat aataaataaaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
1				5				10				15		
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20				25				30		
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35				40				45		
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50				55				60		
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65				70				75		
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80				85				90		
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95				100				105		
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110				115				120		
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125				130				135		
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140				145				150		
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155				160				165		
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His
				170				175				180		
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe
				185				190				195		

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210
Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225
Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240
Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255
Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270
Val Glu Leu

<210> 359
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 359
ccagcagtgc ccatactcca tagc 24

<210> 360
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 360
tgacgagtgg gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 361
gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtggga gcgcggcg 50
ccggcgcccc tggcgagag atcagaagcc tcttccccaa gccgagccaa 100
cctcagcgccc gacccgggct cagggacgcg gcggcgcccc cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcg 200
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tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
ggggccacac tactgtgtcg ttttccact actcccaagg gcaagtgtac 450
cttggaaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550
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caattgggag atttcagaaaa cattccccc accatcattt agaaatggtt 1300
tgccctaattt gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
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tttgcaccct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcaact tcattctgga cacagttgga 1700
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cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15

Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
20 25 30

Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
35 40 45

Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
50 55 60

Lys Ser Thr Ser Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
65 70 75

Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
80 85 90

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
185 190 195

Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
200 205 210

Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
215 220 225

Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
230 235 240

Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
245 250 255

Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
260 265

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccc ccccccgggg cttggcctca agctgcggac gacgcgggg 100
ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcgggggcc 150
tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
agggggcgccg ccccgccgca gtcccccgcg gcccccgacc ctgaggcgtc 250
gcctctggcc gagccgcccc acaggcagtc cctcgccccg tggctccgc 300
agaccccgccg gccggccctgc tccaggtgct tcggccagagc catcgagagc 350
agcccgccgacc tgctgcacag gatcaaggat gaggtggccg caccgggcat 400
agtgggttggaa gtttctgttag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga tggtaaaaaac cgtgttaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
gtggaaagca gggaaactgg atcttgatata tccagtacaa cattatgttc 600
ccgaattccc agaaaaagaa tatgaaggtaaaaaggttgc tgtcacaaca 650
agattactga tttcccattt aagtggaaatt cgtcattatg aaaaggacat 700
aaaaaaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
gattttacta aatttaaaac agagcaggag aatgaagcca aatgccgaa 850
ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
gatcctttgt tcttcaaacc tgtagttagttagt caactttgg 1000
ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050
tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gattacaat agagcaaggt aaatgaatac 1150
cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200
aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacatgg 1250
gagctttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

<210> 366
<211> 373
<212> PRT
<213> Homo sapiens

<400> 366
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
1 5 10 15
Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
20 25 30
Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
35 40 45
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
50 55 60
Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
65 70 75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
80 85 90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
 95 100 105
 Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
 110 115 120
 Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
 125 130 135
 Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
 140 145 150
 Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
 155 160 165
 Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
 170 175 180
 Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
 185 190 195
 Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
 200 205 210
 Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
 215 220 225
 Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
 230 235 240
 Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
 245 250 255
 Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
 260 265 270
 Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn
 275 280 285
 Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
 290 295 300
 Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
 305 310 315
 Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
 320 325 330
 Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
 335 340 345
 Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
 350 355 360
 Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
 365 370

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tgaaaaagaa gtctggtag aaggtagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggctt cattctccctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacacctag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gttcacccat ggttgcttt gccaaattgt gggaaaggagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgtta cgtaagctcg 50

gaattcggct cgaggctggt gggagaaga gcagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgcgtttgc tcatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccggcc gggactggtg cgcgaggggc 200
tggggcggaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc atttgagatc gatgacagtg ccaacttccg gaagcggggc 300
tcactgctct ggaaccagca ggtatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggtatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggtatggcctg 450
gaagctggtg gctatgtctc ctccttgc cctgcgtgtc ccctggtgga 500
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tggtggcgt gtcgggtggt acgcaccccg gggctgccc gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
gcccaccaca gccccaggcc ctgagacggc gccttcatt gagcgcctgg 700
agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800
gtcaggagcg ccagacacccg ggggccaggg tgggggtggg ggtgggggtg 850
gtggtgggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtccccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtccccca gatcgacacg caaaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met Ala Ala Ala Ser Ala Gly Ala Thr Arg Leu Leu Leu Leu Leu
1 5 10 15

Leu Met Ala Val Ala Ala Pro Ser Arg Ala Arg Gly Ser Gly Cys
20 25 30

Arg Ala Gly Thr Gly Ala Arg Gly Ala Gly Ala Glu Gly Arg Glu
35 40 45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
 50 55 60
 Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
 65 70 75
 Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
 80 85 90
 Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
 95 100 105
 Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
 110 115 120
 Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
 125 130 135
 Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
 140 145 150
 Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
 155 160 165
 Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
 170 175 180
 Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
 185 190 195
 Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
 200 205 210
 Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
 215 220 225
 Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
 230 235 240
 Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
 245 250 255
 Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
 260 265

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggAACCCGA GCCGGAGCCG gagccacAGC ggggagggtg 50
 gcctggcggc ctggAGCCGG acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccggggggcc caccatgctg gtgactgcct accttgcttt 150
 tgttaggcctc ctggcctcct gcctggggct ggaactgtca agatGCCGG 200

ctaaacccccc tggaagggcc tgcagcaatc cctccttcct tcggttcaa 250
ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctcttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctcttctcc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500
actactttgt gctgcttagtg gggcgagcac ttgggtggct gtccacagcc 550
ctgctcttct cagccttcga ggcctggtat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc taccttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgttagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgcccgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
cacacggggc ccctctggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct ctcccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagccccatg cacctgctgt cccttgctgt gctcatcgtc gtcttcctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccgggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcctacgga gaaaggtgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttccgg gtacctctgc actcaactggc ttgccttaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagoatttgc tctgctgtca tggtgatggc tctgctggca gtgggtggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgcccctga gctgtaaccc cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggttct cctgccattg ctgggtgttt 1600
gggaggacat gatgggggtg atggactgga aagaagggtgc caaaagttcc 1650

ctctgtgtta ctcccatat gaaaataaac actttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile
						245			250					255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp
						260			265					270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe
						275			280					285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg
						290			295					300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu
						305			310					315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr
						320			325					330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile
						335			340					345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser
						350			355					360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala
						365			370					375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys
						380			385					390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr
						395			400					405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu
						410			415					420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu
						425			430					435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu
						440			445					450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

gcgacgcgca gccccggccggc gagaggaaac gcggcgccgg gcccggcccg 50

gccctggaga tggtccccgg cgccgcggc tggtgtgtc tcgtgctctg 100

gctcccccgcg tgcgtcgccgg cccacggctt ccgtatccat gattatttgt 150

actttcaagt gctgagtcct gggacattc gatacatctt cacagccaca 200

cctgccaagg actttggtgg tatcttcac acaaggtatg agcagattca 250

ccttgtcccc gctgaacctc cagaggcctg cggggaaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccccc 350
ctctccaaga ctcgggtggt ccaggagcac ggccggccgg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca gcgcacagct gacatccccg ccctcttccct gctcggccga 500
gacggctaca ttagccggcg ctctctggaa cagcatgggc tgccatgggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggacccctc tggtagaaga gtttgccttccatccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttggaga tagcatctgg ggacaagtgg agccaggtag agaaaaagg 750
tttggcggtt gctaggctga aagggaaagcc acaccactgg ccttcccttc 800
cccaggccccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggtct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
tacccagggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
aaagagctgg tgtttgggaa ctcaataaac cctcactgac ttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaaaaaaaaaaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
1 5 10 15

Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
20 25 30

Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
35 40 45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
50 55 60

Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
65 70 75

Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
80 85 90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctggatcat ggaacttgca ctgctgtgtg 50
 ggctgggtgatggctggatgtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtcaagca agtactggaaaatgccta tccttccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagaccatg actgctgcta tgaccacctg 250
 aagacccagg ggtgcggcat ctacaaggac aacaacaaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttatgtga 350
 tctatctgaa aatgaggac tccgataaaa aagctattac tawtnaaaa 400
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 450
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
				20					25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
				35					40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
				50					55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
				65					70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
				80					85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
				95					100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
				110					115					

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381
ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382
ctcgcttctt cttctgtggat gggggccca gggggcccagg agagtataaa 50
ggcgatgtgg agggtgccccg gcacaaccag acgcccagtc acaggcgaga 100
gcacctggat gcacccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gccccacactg ggcaggaaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagccta ggtggaaata cccaggaagt 350
cacccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggtatggtc atgtacacca gcaaggaccg ctatttctat 450
tttgggaagc ttgatggcca gatctcctct gcctacccca gccaagaggg 500
gcaggtgctg gtgggcataat atggccagta tcaactcctt ggcataaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaaatc tcacataactc agcaaactca cccgtgggtc gctagggtgg 650
ggtatggggc catccgagct gaggccatct gtgtgggtgg ggctgatgg 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15
Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60

Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75

Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90

Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105

Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120

Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135

Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150

Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165

Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384

<211> 2379

<212> DNA

<213> Homo sapiens

<400> 384

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<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

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					20			25					30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
					35			40					45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
					50			55					60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
					65			70					75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
					80			85					90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
					95			100					105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
					110			115					120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
					125			130					135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
					140			145					150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg
					155			160					165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys
					170			175					180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser
					185			190					195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu

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His Leu Glu His Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe	
215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys	
230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu	
245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly	
260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu	
275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser	
290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu	
305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe	
320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu	
335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile	
350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu	
365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu	
380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly	
395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile	
410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu	
425	430	435
Leu Val Ile Tyr Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys	
440	445	450
Gln Leu Gln Gln Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys	
455	460	465
Arg Gln Ser Leu Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr	
470	475	480
Val Asp Tyr Lys Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu	
485	490	495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

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<210> 387

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

gctgagttta catttacggt ctaactccct gagaaccatc cctgtcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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ttgactgtcc tttaaatatg tcaagatcca gacttttagt tgtcacctca 100

gcgatctcaa cgataggat cttgtgtttt ccgttatcc agttggtgct 150

ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggat atctggatcc tcctgctgct ggtttggtg 250
gcagctttc tctgtggagc tgtggtcctc tgccctccagt gctggctgag 300
gagaccccga attgatttctc acaggcgcac catggcagtt tttgctgttg 350
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atgtttggc ccttttaggct ccccacctcc atatgaagaa attgtaaaaa 500
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taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
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ctgacaaatt tggtaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

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20	.													30
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln
35									40					45
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu
50									55					60
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys
65									70					75
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala
80									85					90
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala
95									100					105
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro
110									115					120
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser
125									130					135
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr				
140									145					
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<212> DNA														
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<223> Synthetic construct.														
<400> 391														
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<210> 392														
<211> 23														
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<213> Artificial														
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<221> Artificial Sequence														
<222> 1-23														
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<400> 392														
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<210> 393														
<211> 47														
<212> DNA														
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<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcgacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

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Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
20 25 30

His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
35 40 45

Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
50 55 60

Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
65 70 75

Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
80 85 90

Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
95 100 105

Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
110 115 120

Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
125 130 135

Ser Gly Ser Ile Arg
140

<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

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<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
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 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser
					155				160				165	
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly
					170				175				180	
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg
					185				190				195	
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu
					200				205				210	
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe
					215				220				225	
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln
					230				235				240	
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly
					245				250				255	
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala
					260				265				270	
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp
					275				280				285	
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu
					290				295				300	
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg
					305				310				315	
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly
					320				325				330	
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser
					335				340				345	
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu							
					350									

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399
ggttggtgcc cgaaagggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400
caaccccaag cttaactggg caggagctga ggtgtttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401
gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttccct 50
gtgggtctga ggggaccaga agggtgagct acgttggctt tctggaagg 100
gaggctatat gcgtcaattc cccaaaacaa gtttgacat ttcccctgaa 150
atgtcattct ctatctattc actgcaagtg cctgctgttc caggcttac 200
ctgctggca ctaacggcg agccaggatg gggacagaat aaaggagcca 250
cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300
ttctcttcac gggaggcttgcagttttc ttactcctgt ggctccaga 350
tttcaggcct aagatgaaag cctcttagtct tgccctcagc ctctctctg 400
ctgcgtttta tctccttatgg actccttcca ctggactgaa gacactcaat 450
ttggaagct gtgtgatcgc cacaacaccc tggaaatac gaaatggatt 500
ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550
gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcaatcga 600
tgctgcctcc tgcccattt gctaagactc tatctggaca gggatattaa 650
aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700
ccaattccctt tcttaccatc aagaaggacc tccggctctc tcattccccac 750

atgacatgcc attgtgggaa ggaagcaatg aagaaataca gccagattct 800
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggcttgg 850
ggaaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
agtatgtctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
acctgcagag gaggcatgac cccaaaccac catctctta ctgtactagt 1000
cttgtgctgg tcacagtgtt tcttattttt gcattacttg cttccttgc 1050
tgattgtctt tatgcattccc caatcttaat tgagaccata ttgtataag 1100
atttttgtaa tatctttctg ctattggata tatttatttag ttaatatatt 1150
tatttatttt ttgctattta atgtattttt tttttactt ggacatgaaa 1200
ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
ctaggggggt tattcatttt tattcaacta aggacatatt tactcatgct 1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
tgtgaaataa gtttgatgt ggaattgcac atctacctta caattactga 1450
ccatccccag tagactcccc agtcccaataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tcttgcata 1550
ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1														15
Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu

5

10

15

20

25

30

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
														45
35														

35

40

45

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
														60
50														

50

55

60

Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
														75
65														

65

70

75

Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
														90
80														

85

90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr		
													95	100	105	
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile		
														110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg		
														125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu		
														140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys		
														155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe		
														170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser		
														185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu		
														200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys		
														215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln		
														230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln		
														245	250	255
Trp	Met	Glu	Glu	Thr	Glu											
														260		

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggc ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 404
agtccctcctt aagatttotga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgtac tgctgaatgt ccgtcccgga ggaggaggag 50
aggctttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggttaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat agggaaatgg tgogcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccggccat ttacagacac gtatgttatt ctggaggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgggtttggc aaaagtgaag atgagcatta 400
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctgtga agttcagat gcaaatggaa 500
ggaaaaagga aacttggaggaaaaccattt cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttggcag 600
gctgggtacc caatatacaa agagcagcac tggtaatat gggagattta 650
accacttatg atacagtgaa acactacttg gtattgaata caccacttga 700
ggacaatatac atgactcactg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggAACACCA gccgatgtca tcaaaAGCAG aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggctg agaatgaccc cttggtaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
 20 25 30
 Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
 35 40 45
 Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
 50 55 60
 Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
 65 70 75
 Leu Gly Ile Ile Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
 80 85 90
 Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
 95 100 105
 Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
 110 115 120
 Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
 125 130 135
 Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 140 145 150
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
 155 160 165
 Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
 170 175 180
 Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
 185 190 195
 Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
 200 205 210
 Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
 215 220 225
 Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
 230 235 240
 Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
 245 250 255
 Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270
 Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285
 Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300
 Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcgatccc gttatcgctc tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cgacgcgtg ggcgcggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctggata 100
cagcatttaa taaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150
tagataattt tcgttggcca gaatgtaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgtcgccaggat attttttttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagccca gaacagttga 300
accatgcctt tcacacatgt ggtgtatccc ccacattggc tttttcatg 350
ataaaatgctg tatccaatgc tcaggtgaga ggtgataatgt atgaaagcgg 400
ctgttttagga agaacaggtg ctcgagtttgc tttttcattt ggtttcatgt 450
tgcgtttgg gtcacttattt gcttccatgt ggattttttt tggtgcatat 500
gttacccaaa atactgtatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcaattata ttttttagca ctctgatcta caaatttggaa agaaccgaag 600
agctatggac ctgagatcac ttcttaagtc acatttcct tttgttatat 650
tctgttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
tagattgtac attaaatgtt ttgtttcttt acattttat gttctgagtt 750
ttgaaaatagt tttatgaaat ttctttatTT ttcattgcat agactgttaa 800
tatgtatata atacaagact atatgaattt gataatgagt atcagtttt 850
tattcctgag atttagaact tgatctactc cctgagccag ggtaacatca 900
tcttgcatt ttagaagtaa ccactcttgc ctctctggct gggcacggtg 950
gctcatgcct gtaatcccag cacttggga ggccgaggcg ggccgattgc 1000
ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaacccccatc 1050
tactaaaaat acaaaaatTA gccaggcatg gtggtgggtg cctgtaatcc 1100
cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
aggttgcagt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
gaagatgtac aaaaaaatAT agttcataat atctggaatg agcactgagc 1300
cataaaaggt tttcagcaag ttgttaacttA ttttggccta aaaatgaggt 1350
ttttttggta aagaaaaat atttggctt atgtattgaa gaagtgtact 1400
tttatataat gatTTTTAA atgccccaaag gactagtttA aaagcttctt 1450
ttaaaaagaa ttcctctaAt atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1 5 10 15

Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
20 25 30

Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
35 40 45

Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60

Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 411

gtttgaggaa gctgggatac 20

<210> 412

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 412

ccaaactcga gcacaccttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-40

<223> Synthetic construct.

<400> 413

atggcaggct tccttagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgcattggca aacttcctca aaggaggggc agagcctgctc cagggcagga 50
gcagctggcc cactggcgcc ccgcaacact ccgtctcacc ctctggccccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccaag ggtgggtggc agctgggtca 200
gggacacctacg gcacacctgctg gaccaccccg cttctccat cgaagcagg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcctt ggcacctcatc 350
tttgccatag tcacgacatg gatgttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggacgcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttc cgtaaaaat ctgcagtggg gccgccaacg tcgtggccccc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atgaaaccac gggagctgtg 650
ctggcacaga aggcatttga catgtactct ggagatgtt a tgcaccttagt 700
gaaattcctt aaagaaattc cgggggggtgc actgggtctg gtggcctcct 750
acgacgatcc agggacccaa atgaacgatg aaagcaggaa actcttctct 800
gacttggggta gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatacgtt gccaagagacc tcagggtaa aagccccctt gaggcattct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgtc 950
gagatggagg gctgcattgcc cccgaagcca ttttagggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
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gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgaa aacagaaccc 1150
tcccacacca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttgcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaat 1300
tatttttqct qtttttqaaa aaaaaaaaaa aaaaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15

Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30

Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45

Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60

Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75

Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90

Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105

Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120

Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135

Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150

Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165

Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180

Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195

Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210

Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgcc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gtcgctcg ctcctctctc tcctctctcac tcctccctcc 200
ctctctctct gcctgtcota gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttgtct ccgcctctct gctggaggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtg ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagccca cggatatgac cagcctggca ccgagcctt 500
ggacotgcac aacaatggcc acacagtgc actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgccc gctccacctg 600
cactgggtc agaaaggatc cccaggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggt gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtgg tgagactaag aatatacgctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccc aacagctggg gcagtacttc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagtttt tatagaaggt cccagattc aatggaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcatgg tcttgcttc 1100
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
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attgctagaa agattcgaa gaagaggctg gaaaaccgaa agagtgtggt 1250
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catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgttagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
ccttccccctg gacatctctt agagaggaat ggacccaggg tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgttagg aggaaatgag 1500
gaaatcgctg tgggttaat gcagaganca aactctgttt agttgcaggg 1550
gaagtttggg atataccca aagtccctcta ccccctcaact tttatggccc 1600
tttccctaga tatactgcgg gatctctcct taggataaaag agttgctgtt 1650
gaagttgtat attttgatc aatatatttg gaaattaaag tttctgactt 1700
t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
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20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala	
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly		
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His		
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala		
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu		
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His		
170	175	180
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro		
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe		
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val		
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln		
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro		
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn		
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr		
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly		
290	295	300
Cys Leu Cys Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile		
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser		
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424

<211> 18

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
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<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgtc 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgtc tggccattat tgtc 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaaccca tgatacccta ctgaacacccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
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acattttgc tcgtggaccc aaaggtagca atctgaaaca tgaggagttac 100
gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcagggaca 200
ctaccaaacc aacagcagtc aaatcaggc tttccttctt taagtctgat 250
accattaaca cagatgctca cactgggcc agatctgcat ctgttaaattc 300
ctgctgcagg aatgacacact ggtacccaga cccacccatt gaccctggga 350
gggttgaatg tacaacagca actgcaccca catgtgttac caattttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgcccggg aggcatcctg 500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggacc ccagcaggcc 600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccacccct 650
gcagggatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
agcaaatgga attcagtaag ctgtttcaaa tttttcaac taagctgcct 750
cgaatttgggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgttag agaatccaa 900
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tatgctgcct ggatgatatg catattaaaa catatttggaa aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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					20					25				30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Ser	Asn	
						35			40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
									55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
									65					75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
							80						90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
							95						105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
							110				115		120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
							125				130		135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
							140			145			150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
							155			160			165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
							170			175			180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
							185			190			195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
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<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ccgcctccag ctccgcgtg cccggcagcc gggagccatg cgaccccagg 150
gccccggcgc ctcccccgcag cggctccgcg gcctcctgct gtcctgctg 200
ctgcagctgc ccgcgcgtc gagcgctct gagatcccc agggaaagca 250
aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacggag ccctggggcc 350
aatgttattc cgggtacacc tggatcccc ggtcggatg gattcaaagg 400
agaaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
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aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgcgttaag 550
agttttgttc agtggctcac ttccgctaaa atgcagaaat gcatgctgtc 600
agcgttggta ttccacattc aatggagctg aatgttcagg acctcttccc 650

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attgaagcta taattttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgactt cttctgtgga aggacttgtt gaaggaattg 750
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ccaaaaggag atgcttctac tggatggaat tcagttctc gcattcattat 850
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ttattatgcc ttggaatggt tcacttaat gacatttaa ataagtttat 950
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<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431
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Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 432
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial Sequence

<400> 432
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<210> 433
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<220>
<223> Synthetic oligonucleotide probe

<400> 433
cgcaggacag ttgtgaaaat a 21

<210> 434
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
atgacgctcg tccaaggcca c 21

<210> 435

<211> 19
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<220>
<223> Synthetic oligonucleotide probe

<400> 435
cccacacctgta ccaccatgt 19

<210> 436
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<220>
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<400> 436
actccaggca ccatctgttc tccc 24

<210> 437
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<400> 437
aagggctggc attcaagtc 19

<210> 438
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<400> 438
tgacctggca aaggaagaa 19

<210> 439
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<220>
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<400> 439
cagccaccct ccagtccaag g 21

<210> 440
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<220>
<223> Synthetic oligonucleotide probe

<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
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<212> DNA
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<220>
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<400> 441
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<210> 442
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<400> 442
tcctccatca cttcccctag ctcca 25

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<400> 443
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<400> 444
aaaggacacc gggatgtg 18

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<400> 445
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<210> 446
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<220>
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<400> 446
caattctgga tgaggtggta ga 22

<210> 447
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<400> 447
caggactgag cgcttgttta 20

<210> 448
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<220>
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<400> 448
caaagcgcca agtaccggac c 21

<210> 449
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<400> 449
ccagacaccta gccaggaa 18

<210> 450
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<400> 450
cccttagctga cccccttca 18

<210> 451
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<212> DNA
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<400> 451
tctgacaaggc agttttctga atc 23

<210> 452
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<400> 452
ctctccccct ccctttccct ttgttt 26

<210> 453
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<212> DNA
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<223> Synthetic oligonucleotide probe

<400> 453
ctctggtgcc cacagtga 18

<210> 454
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<212> DNA
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<400> 454
ccatgcctgc tcagccaaga a 21

<210> 455
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<223> Synthetic oligonucleotide probe

<400> 455
caggaaatct ggaaacctac agt 23

<210> 456
<211> 20
<212> DNA

<213> Artificial Sequence
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<223> Synthetic oligonucleotide probe
<400> 456
ccttgaaaag gacccaggttt 20

<210> 457
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 457
atgagtcgca cctgctgttc cc 22

<210> 458
<211> 18
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<213> Artificial Sequence

<220>
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<400> 458
tagcagctgc ccttggta 18

<210> 459
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe
<400> 459
aacagcaggt gcgactcatc ta 22

<210> 460
<211> 23
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tgctaggcgaa cgacacccag acc 23

<210> 461
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<400> 461
tggacacgtg gcagtgg 18

<210> 462
<211> 19
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<210> 463
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<210> 464
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<400> 466

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<210> 467
<211> 18
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<220>
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<400> 467
gcccgagatc ccacttgt 18

<210> 468
<211> 19
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 468
actgctccgc ctactacga 19

<210> 469
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 469
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<210> 470
<211> 19
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 470
aaggccaagg tgagtccat 19

<210> 471
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 471
cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 472
tcagggtcta catcagcctc ctgc 24

<210> 473
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 473
aaggccaagg tgagtccat 19

<210> 474
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 474
cctactgagg agccctatgc 20

<210> 475
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 475
tccaggtgga cccccacttca gg 22

<210> 476
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 476
gggaggctta taggccccat ctgg 24

<210> 477
<211> 50
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

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